(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 September 2003 (04.09.2003)

PCT

(10) International Publication Number
WO 03/072821 A2

(51) International Patent Classification[7]: C12Q 1/68

(21) International Application Number: PCT/EP03/02035

(22) International Filing Date: 27 February 2003 (27.02.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
02004551.4 27 February 2002 (27.02.2002) EP

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*
— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHOD AND NUCLEIC ACIDS FOR THE ANALYSIS OF A COLON CELL PROLIFERACTIVE DISORDER

(57) Abstract: The present invention relates to modified and genomic sequences, to oligonucleotides and/or PNA-oligomers for detecting the cytosine methylation state of genomic DNA, as well as to a method for ascertaining genetic and/or epigenetic parameters of genes for use in the differentiation, diagnosis, treatment and/or monitoring of colon cell proliferative disorders, or the predisposition to colon cell proliferative disorders.

WO 03/072821 A2

Method and nucleic acids for the analysis of a colon cell proliferative disorder

Field of the Invention

The levels of observation that have been studied by the methodological developments of recent years in molecular biology, are the genes themselves, the translation of these genes into RNA, and the resulting proteins. The question of which gene is switched on at which point in the course of the development of an individual, and how the activation and inhibition of specific genes in specific cells and tissues are controlled is correlatable to the degree and character of the methylation of the genes or of the genome. In this respect, pathogenic conditions may manifest themselves in a changed methylation pattern of individual genes or of the genome.

Colorectal cancer is the fourth leading cause of cancer mortality in men and women, although ranking third in frequency in men and second in women. The 5-year survival rate is 61% over all stages with early detection being a prerequisite for curative therapy of the disease. Up to 95% of all colorectal cancers are adenocarcinomas of varying differentiation grades .

Sporadic colon cancer develops in a multistep process starting with the pathologic transformation of normal colonic epithelium to an adenoma which consecutively progresses to invasive cancer. The progression rate of benign colonic adenomas depends strongly on their histologic appearance: whereas tubular-type adenomas tend to progress to malignant tumors very rarely, villous adenomas, particularly if larger than 2 cm in diameter, have a significant malignant potential.

During progression from benign proliferative lesions to malignant neoplasms several genetic and epigenetic alterations occur. Somatic mutation of the APC gene seems to be one of the earliest events in 75 to 80% of colorectal adenomas and carcinomas. Activation of K-RAS is thought to be a critical step in the progression towards a malignant phenotype. Consecutively, mutations in other oncogenes as well as alterations leading to inactivation of tumour suppressor genes accumulate.

Aberrant DNA methylation within CpG islands is among the earliest and most common alterations in human malignancies leading to abrogation or overexpression of a broad spectrum of genes. In addition, abnormal methylation has been shown to occur in CpG rich regulatory elements in intronic and coding parts of genes for certain tumours. In contrast to the specific hypermethylation of tumour suppressor genes, an overall hypomethylation of DNA can be observed in tumour cells. This decrease in global methylation can be detected early, far before the development of frank tumour formation. Also, correlation between hypomethylation and increased gene expression was reported for many oncogenes. In colon cancer, aberrant DNA methylation constitutes one of the most prominent alterations and inactivates many tumor suppressor genes such as p14ARF, p16INK4a, THBS1, MINT2, and MINT31 and DNA mismatch repair genes such as hMLH1.

In the molecular evolution of colorectal cancer, DNA methylation errors have been suggested to play two distinct roles. In normal colonic mucosa cells, methylation errors accumulate as a function of age or as time-dependent events predisposing these cells to neoplastic transformation. For example, hypermethylation of several loci could be shown to be already present in adenomas, particularly in the tubulovillous and villous subtype. At later stages, increased DNA methylation of CpG islands plays an important role in a subset of tumours affected by the so called CpG island methylator phenotype (CIMP). Most CIMP+ tumours, which constitute about 15% of all sporadic colorectal cancers, are characterised by microsatellite instability (MIN) due to hypermethylation of the hMLH1 promoter and other DNA mismatch repair genes. By contrast, CIMP- colon cancers evolve along a more classic genetic instability pathway (CIN), with a high rate of p53 mutations and chromosomal changes.

However, the molecular subtypes do not only show varying frequencies regarding molecular alterations. According to the presence of either micro satellite instability or chromosomal aberrations, colon cancer can be subclassified into two classes, which also exhibit significant clinical differences. Almost all MIN tumours originate in the proximal colon (ascending and transversum), whereas 70% of CIN tumours are located in the distal colon and rectum. This has been attributed to the varying prevalence of different carcinogens in different sections of the colon. Methylating carcinogens, which constitute the prevailing carcinogen in the proximal colon have been suggested to play a role in the pathogenesis of MIN cancers, whereas CIN tumours are thought to be more frequently caused by adduct-forming carcinogens, which occur more frequently in distal parts of the colon and rectum. Moreover, MIN tumours have a

better prognosis than do tumours with a CIN phenotype and respond better to adjuvant chemotherapy.

The identification of markers for the differentiation of colon carcinoma as well as for early detection are main goals of current research.

5-methylcytosine is the most frequent covalent base modification in the DNA of eukaryotic cells. It plays a role, for example, in the regulation of the transcription, in genetic imprinting, and in tumorigenesis. Therefore, the identification of 5-methylcytosine as a component of genetic information is of considerable interest. However, 5-methylcytosine positions cannot be identified by sequencing since 5-methylcytosine has the same base pairing behaviour as cytosine. Moreover, the epigenetic information carried by 5-methylcytosine is completely lost during PCR amplification.

A relatively new and currently the most frequently used method for analysing DNA for 5-methylcytosine is based upon the specific reaction of bisulfite with cytosine which, upon subsequent alkaline hydrolysis, is converted to uracil which corresponds to thymidine in its base pairing behaviour. However, 5-methylcytosine remains unmodified under these conditions. Consequently, the original DNA is converted in such a manner that methylcytosine, which originally could not be distinguished from cytosine by its hybridisation behaviour, can now be detected as the only remaining cytosine using "normal" molecular biological techniques, for example, by amplification and hybridisation or sequencing. All of these techniques are based on base pairing which can now be fully exploited. In terms of sensitivity, the prior art is defined by a method which encloses the DNA to be analysed in an agarose matrix, thus preventing the diffusion and renaturation of the DNA (bisulfite only reacts with single-stranded DNA), and which replaces all precipitation and purification steps with fast dialysis (Olek A, Oswald J, Walter J. A modified and improved method for bisulphite based cytosine methylation analysis. Nucleic Acids Res. 1996 Dec 15;24(24):5064-6). Using this method, it is possible to analyse individual cells, which illustrates the potential of the method. However, currently only individual regions of a length of up to approximately 3000 base pairs are analysed, a global analysis of cells for thousands of possible methylation events is not possible. However, this method cannot reliably analyse very small fragments from small sample quantities either. These are lost through the matrix in spite of the diffusion protection.

An overview of the further known methods of detecting 5-methylcytosine may be gathered from the following review article: Rein, T., DePamphilis, M. L., Zorbas, H., Nucleic Acids Res. 1998, 26, 2255.

To date, barring few exceptions (e.g., Zeschnigk M, Lich C, Buiting K, Doerfler W, Horsthemke B. A single-tube PCR test for the diagnosis of Angelman and Prader-Willi syndrome based on allelic methylation differences at the SNRPN locus. Eur J Hum Genet. 1997 Mar-Apr;5(2):94-8) the bisulfite technique is only used in research. Always, however, short, specific fragments of a known gene are amplified subsequent to a bisulfite treatment and either completely sequenced (Olek A, Walter J. The pre-implantation ontogeny of the H19 methylation imprint. Nat Genet. 1997 Nov;17(3):275-6) or individual cytosine positions are detected by a primer extension reaction (Gonzalgo ML, Jones PA. Rapid quantitation of methylation differences at specific sites using methylation-sensitive single nucleotide primer extension (Ms-SNuPE). Nucleic Acids Res. 1997 Jun 15;25(12):2529-31, WO 95/00669) or by enzymatic digestion (Xiong Z, Laird PW. COBRA: a sensitive and quantitative DNA methylation assay. Nucleic Acids Res. 1997 Jun 15;25(12):2532-4). In addition, detection by hybridisation has also been described (Olek et al., WO 99/28498).

Further publications dealing with the use of the bisulfite technique for methylation detection in individual genes are: Grigg G, Clark S. Sequencing 5-methylcytosine residues in genomic DNA. Bioessays. 1994 Jun;16(6):431-6, 431; Zeschnigk M, Schmitz B, Dittrich B, Buiting K, Horsthemke B, Doerfler W. Imprinted segments in the human genome: different DNA methylation patterns in the Prader-Willi/Angelman syndrome region as determined by the genomic sequencing method. Hum Mol Genet. 1997 Mar;6(3):387-95; Feil R, Charlton J, Bird AP, Walter J, Reik W. Methylation analysis on individual chromosomes: improved protocol for bisulphite genomic sequencing. Nucleic Acids Res. 1994 Feb 25;22(4):695-6; Martin V, Ribieras S, Song-Wang X, Rio MC, Dante R. Genomic sequencing indicates a correlation between DNA hypomethylation in the 5' region of the pS2 gene and its expression in human breast cancer cell lines. Gene. 1995 May 19;157(1-2):261-4; WO 97/46705 and WO 95/15373.

An overview of the Prior Art in oligomer array manufacturing can be gathered from a special edition of Nature Genetics (Nature Genetics Supplement, Volume 21, January 1999), published in January 1999, and from the literature cited therein.

Fluorescently labelled probes are often used for the scanning of immobilised DNA arrays. The simple attachment of Cy3 and Cy5 dyes to the 5'-OH of the specific probe are particularly suitable for fluorescence labels. The detection of the fluorescence of the hybridised probes may be carried out, for example via a confocal microscope. Cy3 and Cy5 dyes, besides many others, are commercially available.

Matrix Assisted Laser Desorption Ionization Mass Spectrometry (MALDI-TOF) is a very efficient development for the analysis of biomolecules (Karas M, Hillenkamp F. Laser desorption ionisation of proteins with molecular masses exceeding 10,000 daltons. Anal Chem. 1988 Oct 15;60(20):2299-301). An analyte is embedded in a light-absorbing matrix. The matrix is evaporated by a short laser pulse thus transporting the analyte molecule into the vapour phase in an unfragmented manner. The analyte is ionised by collisions with matrix molecules. An applied voltage accelerates the ions into a field-free flight tube. Due to their different masses, the ions are accelerated at different rates. Smaller ions reach the detector sooner than bigger ones.

MALDI-TOF spectrometry is excellently suited to the analysis of peptides and proteins. The analysis of nucleic acids is somewhat more difficult (Gut I G, Beck S. DNA and Matrix Assisted Laser Desorption Ionisation Mass Spectrometry. Current Innovations and Future Trends. 1995, 1; 147-57). The sensitivity to nucleic acids is approximately 100 times worse than to peptides and decreases disproportionally with increasing fragment size. For nucleic acids having a multiply negatively charged backbone, the ionisation process via the matrix is considerably less efficient. In MALDI-TOF spectrometry, the selection of the matrix plays an eminently important role. For the desorption of peptides, several very efficient matrixes have been found which produce a very fine crystallisation. There are now several responsive matrixes for DNA, however, the difference in sensitivity has not been reduced. The difference in sensitivity can be reduced by chemically modifying the DNA in such a manner that it becomes more similar to a peptide. Phosphorothioate nucleic acids in which the usual phosphates of the backbone are substituted with thiophosphates can be converted into a charge-neutral DNA using simple alkylation chemistry (Gut IG, Beck S. A procedure for selective DNA alkylation and detection by mass spectrometry. Nucleic Acids Res. 1995 Apr 25;23(8):1367-73). The coupling of a charge tag to this modified DNA results in an increase in sensitivity to the same level as that found for peptides. A further advantage of charge tag-

ging is the increased stability of the analysis against impurities which make the detection of unmodified substrates considerably more difficult.

Genomic DNA is obtained from DNA of cell, tissue or other test samples using standard methods. This standard methodology is found in references such as Sambrook, Fritsch and Maniatis eds., Molecular Cloning: A Laboratory Manual, 1989.

Description

The invention provide a method for the analysis of biological samples for features associated with the development of colon cell proliferative disorders, characterised in that the nucleic acid of at least one member of the group comprising MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F, ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR, EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2, ESR1, CASP8, RASSF1, MSH4, MSH5 is/are contacted with a reagent or series of reagents capable of distinguishing between methylated and non methylated CpG dinucleotides within the genomic sequence of interest.

The present invention makes available a method for ascertaining genetic and/or epigenetic parameters of genomic DNA. The method is for use in the improved diagnosis, treatment and monitoring of colon cell proliferative disorders, more specifically by enabling the improved identification of and differentiation between subclasses of said disorder and the genetic predisposition to said disorders. The invention presents improvements over the state of the art in that it enables a highly specific classification of colon carcinomas, thereby allowing for improved and informed treatment of patients.

In a particularly preferred embodiment the present invention makes available methods and nucleic acids that allow the differentiation between colon carcinoma, colon adenoma and normal colon tissue.

Furthermore, the method enables the analysis of cytosine methylations and single nucleotide polymorphisms.

The genes that form the basis of the present invention can be used to form a "gene panel", i.e. a collection comprising the particular genetic sequences of the present invention and/or their respective informative methylation sites. The formation of gene panels allow for a quick and specific analysis of the disorders they are related with. The gene panels described in this invention can be used with surprisingly high efficiency for the diagnosis, treatment and monitoring of and the analysis of colon cell proliferative disorders as described herein. The use of multiple CpG sites from a diverse array of genes, allows for a relatively high degree of sensitivity and specificity in comparison to single gene diagnostic and detection tools. Furthermore, the panel as described herein may be adapted for use in the analysis of many aspects of colon cell proliferative disorders.

In a preferred embodiment, the method comprises the following steps:
In the first step of the method the genomic DNA sample must be isolated from tissue or cellular sources. Such sources may include colon tissue samples, cell lines, histological slides, body fluids, or tissue embedded in paraffin. Extraction may be by means that are standard to one skilled in the art, these include the use of detergent lysates, sonification and vortexing with glass beads. Once the nucleic acids have been extracted the genomic double stranded DNA is used in the analysis.

In a preferred embodiment the DNA may be cleaved prior to the next step of the method, this may be by any means standard in the state of the art, in particular, but not limited to, with restriction endonucleases.

In the second step of the method, the genomic DNA sample is treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridisation behaviour. This will be understood as 'pretreatment' hereinafter.

The above described treatment of genomic DNA is preferably carried out with bisulfite (sulfite, disulfite) and subsequent alkaline hydrolysis which results in a conversion of non-methylated cytosine nucleobases to uracil or to another base which is dissimilar to cytosine in

terms of base pairing behaviour. If bisulfite solution is used for the reaction, then an addition takes place at the non-methylated cytosine bases. Moreover, a denaturating reagent or solvent as well as a radical interceptor must be present. A subsequent alkaline hydrolysis then gives rise to the conversion of non-methylated cytosine nucleobases to uracil. The chemically converted DNA is then used for the detection of methylated cytosines.

Fragments of the pretreated DNA are amplified, using sets of primer oligonucleotides according to SEQ ID NO: 389 to SEQ ID NO: 518, and a, preferably heat-stable, polymerase. Because of statistical and practical considerations, preferably more than ten different fragments having a length of 100 - 2000 base pairs are amplified. The amplification of several DNA segments can be carried out simultaneously in one and the same reaction vessel. Usually, the amplification is carried out by means of a polymerase chain reaction (PCR).

The method may also be enabled by the use of alternative primers, the design of such primers is obvious to one skilled in the art. These should include at least two oligonucleotides whose sequences are each reverse complementary or identical to an at least 18 base-pair long segment of the base sequences specified in the appendix (SEQ ID NO: 133 to SEQ ID NO: 388). Said primer oligonucleotides are preferably characterised in that they do not contain any CpG dinucleotides. In a particularly preferred embodiment of the method, the sequence of said primer oligonucleotides are designed so as to selectively anneal to and amplify, only the colon tissue specific DNA of interest, thereby minimising the amplification of background or non relevant DNA. In the context of the present invention, background DNA is taken to mean genomic DNA which does not have a relevant tissue specific methylation pattern, in this case, the relevant tissue being colon, both healthy and diseased.

According to the present invention, it is preferred that at least one primer oligonucleotide is bound to a solid phase during amplification. The different oligonucleotide and/or PNA-oligomer sequences can be arranged on a plane solid phase in the form of a rectangular or hexagonal lattice, the solid phase surface preferably being composed of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, or gold, it being possible for other materials such as nitrocellulose or plastics to be used as well.

The fragments obtained by means of the amplification can carry a directly or indirectly detectable label. Preferred are labels in the form of fluorescence labels, radionuclides, or detach-

able molecule fragments having a typical mass which can be detected in a mass spectrometer, it being preferred that the fragments that are produced have a single positive or negative net charge for better detectability in the mass spectrometer. The detection may be carried out and visualised by means of matrix assisted laser desorption/ionisation mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI).

The amplificates obtained in the second step of the method are subsequently hybridised to an array or a set of oligonucleotides and/or PNA probes. In this context, the hybridisation preferably takes place in the manner described as follows. The set of probes used during the hybridisation is preferably composed of at least 10 oligonucleotides or PNA-oligomers. However, it is understood and as well claimed, that the process can be conducted using only one Oligonucleotide or PNA probe. In the process, the amplificates hybridise to oligonucleotides previously bonded to a solid phase. In a particularly preferred embodiment, the oligonucleotides are taken from the group comprising SEQ ID NO: 519 to SEQ ID NO: 1030. In a further preferred embodiment the oligonucleotides are taken from the group comprising SEQ ID NO: 895 to SEQ ID NO: 1030. The non-hybridised fragments are subsequently removed. Said oligonucleotides contain at least one base sequence having a length of 10 nucleotides which is reverse complementary or identical to a segment of the base sequences specified in the appendix, the segment containing at least one CpG or TpG dinucleotide. In a further preferred embodiment the cytosine of the CpG dinucleotide, or in the case of TpG, the thiamine, is the 5^{th} to 9^{th} nucleotide from the 5'-end of the 10-mer. One oligonucleotide exists for each CpG or TpG dinucleotide.

In the fifth step of the method, the non-hybridised amplificates are removed.

In the final step of the method, the hybridised amplificates are detected. In this context, it is preferred that labels attached to the amplificates are identifiable at each position of the solid phase at which an oligonucleotide sequence is located.

According to the present invention, it is preferred that the labels of the amplificates are fluorescence labels, radionuclides, or detachable molecule fragments having a typical mass which can be detected in a mass spectrometer. The mass spectrometer is preferred for the detection of the amplificates, fragments of the amplificates or of probes which are complementary to the amplificates, it being possible for the detection to be carried out and visualised by means

of matrix assisted laser desorption/ionisation mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The produced fragments may have a single positive or negative net charge for better detectability in the mass spectrometer.

The aforementioned method is preferably used for ascertaining genetic and/or epigenetic parameters of genomic DNA.

In order to enable this method, the invention further provides the modified DNA of genes MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F, ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR, EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2 , ESR1, CASP8, RASSF1, MSH4, MSH5 as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations within said genes. The present invention is based on the discovery that genetic and epigenetic parameters and, in particular, the cytosine methylation patterns of genomic DNA are particularly suitable for improved diagnosis, treatment and monitoring of colon cell proliferative disorders. Furthermore, the invention enables the differentiation between different subclasses of colon cell proliferative disorders or detection of a predisposition to colon cell proliferative disorders.

The nucleic acids according to the present invention can be used for the analysis of genetic and/or epigenetic parameters of genomic DNA.

This objective is achieved according to the present invention using a nucleic acid containing a sequence of at least 18 bases in length of the pretreated genomic DNA according to one of SEQ ID NO: 133 to SEQ ID NO: 388 and sequences complementary thereto.
The modified nucleic acid could heretofore not be connected with the ascertainment of disease relevant genetic and epigenetic parameters.

The object of the present invention is further achieved by an oligonucleotide or oligomer for the analysis of pretreated DNA, for detecting the genomic cytosine methylation state, said oligonucleotide containing at least one base sequence having a length of at least 10 nucleo-

tides which hybridises to a pretreated genomic DNA according to SEQ ID NO: 133 through to SEQ ID NO: 388. The oligomer probes according to the present invention constitute important and effective tools which, for the first time, make it possible to ascertain specific genetic and epigenetic parameters during the analysis of biological samples for features associated with the development of colon cell proliferative disorders. Said oligonucleotides allow the improved diagnosis, treatment and monitoring of colon cell proliferative disorders and detection of the predisposition to said disorders. Furthermore, they allow the differentiation of different subclasses of colon cell proliferative disorders. The base sequence of the oligomers preferably contains at least one CpG or TpG dinucleotide. The probes may also exist in the form of a PNA (peptide nucleic acid) which has particularly preferred pairing properties. Particularly preferred are oligonucleotides according to the present invention in which the cytosine of the CpG dinucleotide is the 5^{th} - 9^{th} nucleotide from the 5'-end of the 13-mer; in the case of PNA-oligomers, it is preferred for the cytosine of the CpG dinucleotide to be the 4^{th} - 6^{th} nucleotide from the 5'-end of the 9-mer.

The oligomers according to the present invention are normally used in so called "sets" which contain at least one oligomer for each of the CpG dinucleotides within SEQ ID NO: 133 through SEQ ID NO: 388. Preferred is a set which contains at least one oligomer for each of the CpG dinucleotides, from SEQ ID NO: 519 to SEQ ID NO: 1030. Further preferred is a set comprising SEQ ID NO: 895 to SEQ ID NO: 1030.

In the case of the sets of oligonucleotides according to the present invention, it is preferred that at least one oligonucleotide is bound to a solid phase. It is further preferred that all the oligonucleotides of one set are bound to a solid phase.

The present invention moreover relates to a set of preferably at least 10 n (oligonucleotides and/or PNA-oligomers) used for detecting the cytosine methylation state of genomic DNA using treated versions of said genomic DNA (according to SEQ ID NO: 133 to SEQ ID NO: 388 and sequences complementary thereto). However, it is understood and as well claimed, that the process can be conducted using only one Oligonucleotide or PNA oligomer. These probes enable improved diagnosis, treatment and monitoring of colon cell proliferative disorders. In particular they enable the differentiation between different sub classes of colon cell proliferative disorders and the detection of a predisposition to said disorders. In a particularly preferred embodiment the set comprises SEQ ID NO: 519 to SEQ ID NO: 1030.

The set of oligomers may also be used for detecting single nucleotide polymorphisms (SNPs) using pretreated genomic DNA according to one of SEQ ID NO: 133 to SEQ ID NO: 388.

According to the present invention, it is preferred that an arrangement of different oligonucleotides and/or PNA-oligomers (a so-called "array") made available by the present invention is present in a manner that it is likewise bound to a solid phase. This array of different oligonucleotide- and/or PNA-oligomer sequences can be characterised in that it is arranged on the solid phase in the form of a rectangular or hexagonal lattice. The solid phase surface is preferably composed of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, or gold. However, nitrocellulose as well as plastics such as nylon which can exist in the form of pellets or also as resin matrices are suitable alternatives.

Therefore, a further subject matter of the present invention is a method for manufacturing an array fixed to a carrier material for the improved diagnosis, treatment and monitoring of colon cell proliferative disorders, the differentiation between different subclasses of colon cell proliferative disorders and/or detection of the predisposition to colon cell proliferative disorders. In said method at least one oligomer according to the present invention is coupled to a solid phase. Methods for manufacturing such arrays are known, for example, from Patent US 5,744,305 by means of solid-phase chemistry and photolabile protecting groups.

A further subject matter of the present invention relates to a DNA chip for the improved diagnosis, treatment and monitoring of colon cell proliferative disorders. Furthermore the DNA chip enables detection of the predisposition to colon cell proliferative disorders and the differentiation between different subclasses of colon cell proliferative disorders. The DNA chip contains at least one nucleic acid according to the present invention. DNA chips are known, for example, in Patent US 5,837,832.

Moreover, a subject matter of the present invention is a kit which may be composed, for example, of a bisulfite-containing reagent, a set of primer oligonucleotides containing at least two oligonucleotides whose sequences in each case correspond or are complementary to a 18 base long segment of the base sequences specified in the appendix (SEQ ID NO: 133 to SEQ ID NO: 388), oligonucleotides and/or PNA-oligomers as well as instructions for carrying out

and evaluating the described method. However, a kit along the lines of the present invention can also contain only part of the aforementioned components.

The oligomers according to the present invention or arrays thereof as well as a kit according to the present invention are intended to be used for the improved diagnosis, treatment and monitoring of colon cell proliferative disorders. Furthermore the use of said inventions extends to the differentiation between different subclasses of colon cell proliferative disorders and detection of the predisposition to colon cell proliferative disorders. According to the present invention, the method is preferably used for the analysis of important genetic and/or epigenetic parameters within genomic DNA, in particular for use in improved diagnosis, treatment and monitoring of colon cell proliferative disorders, detection of the predisposition to said disorders and the differentiation between subclasses of said disorders.

The methods according to the present invention are used, for example, for improved diagnosis, treatment and monitoring of colon cell proliferative disorders progression, detection of the predisposition to said disorders and the differentiation between subclasses of said disorders.
A further embodiment of the invention is a method for the analysis of the methylation status of genomic DNA without the need for pretreatment. In the first step of the method the genomic DNA sample must be isolated from tissue or cellular sources. Such sources may include cell lines, histological slides, body fluids, or tissue embedded in paraffin. Extraction may be by means that are standard to one skilled in the art, these include the use of detergent lysates, sonification and vortexing with glass beads. Once the nucleic acids have been extracted the genomic double stranded DNA is used in the analysis.

In a preferred embodiment the DNA may be cleaved prior to the treatment, this may be any means standard in the state of the art, in particular with restriction endonucleases. In the second step, the DNA is then digested with one or more methylation sensitive restriction enzymes. The digestion is carried out such that hydrolysis of the DNA at the restriction site is informative of the methylation status of a specific CpG dinucleotide.

In the third step the restriction fragments are amplified. In a preferred embodiment this is carried out using a polymerase chain reaction.

In the final step the amplificates are detected. The detection may be by any means standard in the art, for example, but not limited to, gel electrophoresis analysis, hybridisation analysis, incorporation of detectable tags within the PCR products, DNA array analysis, MALDI or ESI analysis.

The present invention moreover relates to the diagnosis and/or prognosis of events which are disadvantageous or relevant to patients or individuals in which important genetic and/or epigenetic parameters within genomic DNA, said parameters obtained by means of the present invention may be compared to another set of genetic and/or epigenetic parameters, the differences serving as the basis for the diagnosis and/or prognosis of events which are disadvantageous or relevant to patients or individuals.

In the context of the present invention the term "hybridisation" is to be understood as a bond of an oligonucleotide to a completely complementary sequence along the lines of the Watson-Crick base pairings in the sample DNA, forming a duplex structure.

In the context of the present invention, "genetic parameters" are mutations and polymorphisms of genomic DNA and sequences further required for their regulation. To be designated as mutations are, in particular, insertions, deletions, point mutations, inversions and polymorphisms and, particularly preferred, SNPs (single nucleotide polymorphisms).

In the context of the present invention „methylation state analysis" is taken to mean the analysis of cytosines within a nucleic acid in order to ascertain whether they are methylated or not. In the context of the present invention, "epigenetic parameters" are, in particular, cytosine methylations and further modifications of DNA bases of genomic DNA and sequences further required for their regulation. Further epigenetic parameters include, for example, the acetylation of histones which, cannot be directly analysed using the described method but which, in turn, correlates with the DNA methylation.

In the following, the present invention will be explained in greater detail on the basis of the sequences and examples without being limited thereto.

SEQ ID NO: 1 to SEQ ID NO: 64 represent 5' and/or regulatory regions of the genomic DNA of genes MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F,

ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR, EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2, ESR1, CASP8, RASSF1, MSH4, MSH5. These sequences are derived from the ensembl database (date 01.10.2001) (http://www.ensembl.org) and will be taken to include all minor variations of the sequence material which are currently unforeseen, for example, but not limited to, minor deletions and SNPs.

SEQ ID 133 to 388 exhibit the pretreated sequences of DNA derived from genes MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F, ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR, EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2, ESR1, CASP8, RASSF1, MSH4, MSH5. These sequences will be taken to include all minor variations of the sequence material which are currently unforeseen, for example, but not limited to, minor deletions and SNPs.

SEQ ID NO: 389 to SEQ ID NO: 518 exhibit the sequences of primer oligonucleotides for the amplification of pretreated DNA according to Sequence ID NO: 133 to SEQ ID NO: 388.

SEQ ID NO: 65 to SEQ ID NO: 132 exhibit the sequences of oligomers which are useful for the analysis of CpG positions within genomic DNA according to SEQ ID NO: 1 to SEQ ID NO: 64.

SEQ ID NO: 519 to SEQ ID NO: 1030 exhibit the sequences of oligomers which are useful for the analysis of the methylation status of CpG positions within genomic DNA according to SEQ ID NO: 1 to SEQ ID NO: 64 after treatment of said genomic DNA with bisulfite.

SEQ ID NO: 895 to SEQ ID NO: 1030 exhibit the sequences of oligomers which are particularly useful for the analysis of CpG positions within genomic DNA according to SEQ ID NO:

1 to SEQ ID NO: 64, after treatment of said with bisulfite and are subject to a preferred embodiment of this invention.

Description of figures

Figure 1: Differentiation between healthy colon tissue and adenoma or carcinoma colon tissue according to Example 2. The labels on the left side of the plot are gene and CpG identifiers, these can be cross referenced using Table 3 and Table 7. The labels on the right side of the figure give the significance (p-value, T-test) of the difference between the means of the two groups. Each row corresponds to a single CpG and each column to the methylation levels of one sample. CpGs are ordered according to their contribution to the differentiation between the two tissue types (A = healthy, B = non healthy) with increasing contribution from top to bottom. Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in grey, from light (low proportion of methylation) to dark (high proportion of methylation).

Figure 2: Differentiation between healthy colon tissue and carcinoma colon tissue according to Example 2. The labels on the left side of the plot are gene and CpG identifiers, these can be cross referenced using Table 4 and Table 7. The labels on the right side of the figure give the significance (p-value, T-test) of the difference between the means of the two groups. Each row corresponds to a single CpG and each column to the methylation levels of one sample. CpGs are ordered according to their contribution to the differentiation between the two tissue types (A = healthy, B = carcinoma) with increasing contribution from top to bottom. Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in grey, from light (low proportion of methylation) to dark (high proportion of methylation).

Figure 3: Differentiation between healthy colon tissue and adenoma colon tissue according to Example 2. The labels on the left side of the plot are gene and CpG identifiers, these can be cross referenced in Table 5 and Table 7. The labels on the right side give the significance (p-value, T-test) of the difference between the means of the two groups. Each row corresponds to a single CpG and each column to the methylation levels of one sample. CpGs are ordered according to their contribution to the distinction to the differential diagnosis between the two tissue types (A = healthy, B = adenoma) with increasing contribution from top to bottom.

Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in grey, from light (low proportion of methylation) to dark (high proportion of methylation). Due to formatting of the page only 40 CpGs are shown in this figure.

Figure 4: Differentiation between carcinoma colon tissue and adenoma colon tissue according to Example 2. The labels on the left side of the plot are gene and CpG identifiers, these can be cross referenced in Table 6 and Table 7. The labels on the right side give the significance (p-value, T-test) of the difference between the means of the two groups. Each row corresponds to a single CpG and each column to the methylation levels of one sample. CpGs are ordered according to their contribution to the distinction to the differential diagnosis between the two tissue types (A = carcinoma, B = adenoma) with increasing contribution from top to bottom. Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in grey, from light (low proportion of methylation) to dark (high proportion of methylation).

Examples 1 and 2: Digital Phenotype

In the following examples, multiplex PCR was carried out upon tissue samples originating from colon adenomas or colon carcinoma. Multiplex PCR was also carried out upon healthy colon tissue. Each sample was treated in the manner described below in Example 1 in order to deduce the methylation status of CpG positions, the CpG methylation information for each sample was collated and then used in an analysis, as detailed in Example 2. An alternative method for the analysis of CpG methylation status is described in Example 3.

Example 1

In the first step the genomic DNA was isolated from the cell samples using the Wizzard kit from (Promega).

The isolated genomic DNA from the samples are treated using a bisulfite solution (hydrogen sulfite, disulfite). The treatment is such that all non methylated cytosines within the sample are converted to thiamidine, conversely 5-methylated cytosines within the sample remain unmodified.

The treated nucleic acids were then amplified using multiplex PCRs, amplifying 8 fragments per reaction with Cy5 fluorescently labelled primers. PCR primers used are described in Table 1. PCR conditions were as follows.

Reaction solution:

10 ng bisulfite treated DNA

3,5 mM MgCl2

400 µM dNTPs

2 pmol each primer

1 U Hot Star Taq (Qiagen)

Forty cycles were carried out as follows. Denaturation at 95°C for 15 min, followed by annealing at 55°C for 45 sec., primer elongation at 65°C for 2 min. A final elongation at 65°C was carried out for 10 min.

All PCR products from each individual sample were then hybridised to glass slides carrying a pair of immobilised oligonucleotides for each CpG position under analysis. Each of these detection oligonucleotides was designed to hybridise to the bisulphite converted sequence around one CpG site which was either originally unmethylated (TG) or methylated (CG). See Table 2 for further details of all hybridisation oligonucleotides used (both informative and non-informative) Hybridisation conditions were selected to allow the detection of the single nucleotide differences between the TG and CG variants.

5 µl volume of each multiplex PCR product was diluted in 10 x Ssarc buffer (10 x Ssarc:230 ml 20 x SSC, 180 ml sodium lauroyl sarcosinate solution 20%, dilute to 1000 ml with dH2O). The reaction mixture was then hybridised to the detection oligonucleotides as follows. Denaturation at 95°C, cooling down to 10 °C, hybridisation at 42°C overnight followed by washing with 10 x Ssarc and dH2O at 42°C.

Fluorescent signals from each hybridised oligonucleotide were detected using genepix scanner and software. Ratios for the two signals (from the CG oligonucleotide and the TG oligonucleotide used to analyse each CpG position) were calculated based on comparison of intensity of the fluorescent signals.

Example 2

The data obtained according to Example 1 is then sorted into a ranked matrix (as shown in Figures 1 to 4) according to CpG methylation differences between the two classes of tissues, using an algorithm. The most significant CpG positions are at the bottom of the matrix with significance decreasing towards the top. Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in grey, from light (low proportion of methylation) to dark (high proportion of methylation). Each row represents one specific CpG position within a gene and each column shows the methylation profile for the different CpGs for one sample. On the left side a CpG and gene identifier is shown this may be cross referenced with the accompanying tables (Table 1 and 7) in order to ascertain the gene in question and the detection oligomer used. On the right side p values for the individual CpG positions are shown. The p values are the probabilities that the observed distribution occurred by chance in the data set.

For selected distinctions, we trained a learning algorithm (support vector machine, SVM). The SVM (as discussed by F. Model,P. Adorjan,A. Olek,C. Piepenbrock, Feature selection for DNA methylation based cancer classification. Bioinformatics. 2001 Jun;17 Suppl 1:S157-64) constructs an optimal discriminant between two classes of given training samples. In this case each sample is described by the methylation patterns (CG/TG ratios) at the investigated CpG sites. The SVM was trained on a subset of samples of each class, which were presented with the diagnosis attached. Independent test samples, which were not shown to the SVM before were then presented to evaluate, if the diagnosis can be predicted correctly based on the predictor created in the training round. This procedure was repeated several times using different partitions of the samples, a method called cross-validation. Please note that all rounds are performed without using any knowledge obtained in the previous runs. The number of correct classifications was averaged over all runs, which gives a good estimate of our test accuracy (percent of correct classified samples over all rounds).

Healthy colon tissue compared to non healthy colon tissue (colon adenoma and colon carcinoma) (Figure 1)

Figure 1 shows the differentiation of healthy tissue from non healthy tissue wherein the non healthy specimens are obtained from either colon adenoma or colon carcinoma tissue. The evaluation is carried out using informative CpG positions from 27 genes. Informative CpG positions are further described in Table 3.

Healthy colon tissue compared to colon carcinoma tissue (Figure 2)

Figure 2 shows the differentiation of healthy tissue from carcinoma tissue using informative CpG positions from 15 genes. Informative CpG positions are further described in Table 4.

Healthy colon tissue compared to colon adenoma tissue (Figure 3)

Figure 3 shows the differentiation of healthy tissue from adenoma tissue using informative CpG positions from 40 genes. Informative CpG positions are further described in Table 5.

Colon carcinoma tissue compared to colon adenoma tissue (Figure 4)

Figure 4 shows the differentiation of carcinoma tissue from adenoma tissue using informative CpG positions from 2 genes. Informative CpG positions are further described in Table 6.

Example 3: Identification of the methylation status of a CpG site within the gene CD44.

A fragment of the bisulfite treated DNA of the gene CD44 (Seq ID NO: 20) was PCR amplified using primers GAAAGGAGAGGTTAAAGGTTG (Seq ID NO 429) and AACTCACTTAACTCCAATCCC (Seq ID NO 430). The resultant fragment (696 bp in length) contained an informative CpG at position 235. The amplificate DNA was digested with the restriction endonuclease *Apa I*, recognition site GGGCC. Hydrolysis by said endonuclease is blocked by methylation of the CpG at position 235 of the amplificate. The digest was used as a control.

Genomic DNA was isolated from sample using the DNA wizzard DNA isolation kit (Promega). Each sample was digested using *Apa I* according to manufacturer's recommendations (New England Biolabs).

10 ng of each genomic digest was then amplified using PCR primers GAAAGGAGAGGTTAAAGGTTG and AACTCACTTAACTCCAATCCC. The PCR reactions were performed using a thermocycler (Eppendorf GmbH) using 10 ng of DNA, 6 pmol of each primer, 200 µM of each dNTP, 1.5 mM MgCl2 and 1 U of HotstartTaq (Qiagen AG). The other conditions were as recommended by the Taq polymerase manufacturer. Using the above mentioned primers, gene fragments were amplified by PCR performing a first denaturation step for 14 min at 96 °C, followed by 30 - 45 cycles (step 2: 60 sec at 96°C, step 3: 45 sec at 52°C , step 4: 75 sec at 72°C) and a subsequent final elongation of 10 min at 72°C. The presence of PCR products was analysed by agarose gel electrophoresis.

PCR products were detectable with *Apa I* hydrolysed DNA isolated wherein the CpG position in question was up-methylated, when step 2 to step 4 of the cycle program were repeated 34, 37, 39, 42 and 45 fold. In contrast PCR products were only detectable with *Apa I* hydrolysed DNA isolated from down-methylated DNA (and control DNA) when step 2 to step 4 of the cycle program were repeated 42 and 45 fold. These results were incorporated into a CpG methylation matrix analysis as described in Example 2.

Tables

Table 1: PCR primers and products

No:	*Gene:*	*Primer:*	*Amplificate Length:*
1	MDR1 (SEQ ID NO: 1)	TAAGTATGTTGAAGAAAGATTATTGTAG (SEQ ID NO: 389) TAAAAACTATCCCATAATAACTCCCAAC (SEQ ID NO: 390)	633
2	APOC2 (SEQ ID NO: 2)	ATGAGTAGAAGAGGTGATAT (SEQ ID NO: 391) CCCTAAATCCCTTTCTTACC (SEQ ID NO: 392)	533
3	CACNA1G (SEQ ID NO: 3)	GGGATTTAAGAGAAATTGAGGTA (SEQ ID NO: 393) AAACCCCAAACATCCTTTAT (SEQ ID NO: 394)	707
4	EGR4 (SEQ ID NO: 4)	AGGGGGATTGAGTGTTAAGT (SEQ ID NO: 395) CCCAAACATAAACACAAAAT (SEQ ID NO: 396)	293
5	AR (SEQ ID NO: 5)	GTAGTAGTAGTAGTAAGAGA (SEQ ID NO: 397) ACCCCCTAAATAATTATCCT (SEQ ID NO: 398)	460
6	RB1 (SEQ ID NO: 6)	TTTAAGTTTGTTTTTGTTTTGGT (SEQ ID NO: 399) TCCTACTCTAAATCCTCCTCAA (SEQ ID NO: 400)	718
7	GPIb beta (SEQ ID NO: 7)	GGTGATAGGAGAATAATGTTGG (SEQ ID NO: 401) TCTCCCAACTACAACCAAAC (SEQ ID NO: 402)	379
8	MYOD1 (SEQ ID NO: 8)	ATTAGGGGTATAGAGGAGTATTGA (SEQ ID NO: 403) CTTACAAACCCACAATAAACAA (SEQ ID NO: 404)	883
9	WT1 (SEQ ID NO: 9)	AAAGGGAAATTAAGTGTTGT (SEQ ID NO: 405)	747

No:	*Gene:*	*Primer:*	*Amplificate Length:*
		TAACTACCCTCAACTTCCC (SEQ ID NO: 406)	
10	HLA-F (SEQ ID NO: 10)	TTGTTGTTTTTAGGGGTTTTGG (SEQ ID NO: 407) TCCTTCCCATTCTCCAAATATC (SEQ ID NO: 408)	946
11	ELK1 (SEQ ID NO: 11)	AAGTGTTTTAGTTTTTAATGGGTA (SEQ ID NO: 409) CAAACCCAAAACTCACCTAT (SEQ ID NO: 410)	966
12	APC (SEQ ID NO: 12)	TCAACTACCATCAACTTCCTTA (SEQ ID NO: 411) AATTTATTTTTAGTGTTGTAGTGGG (SEQ ID NO: 412)	491
13	BCL2 (SEQ ID NO: 13)	GTATTTTATGTTAAGGGGGAAA (SEQ ID NO: 413) AAAAACCACAATCCTCCC (SEQ ID NO: 414)	640
14	CALCA (SEQ ID NO: 14)	GTTTTGGAAGTATGAGGGTG (SEQ ID NO: 415) CCAAATTCTAAACCAATTTCC (SEQ ID NO: 416)	614
15	CDH1 (SEQ ID NO: 15)	GAGGTTGGGGTTAGAGGAT (SEQ ID NO: 417) CAAACTCACAAATACTTTACAATTC (SEQ ID NO: 418)	478
16	CDKN1A (SEQ ID NO: 16)	GGATTAGTGGGAATAGAGGTG (SEQ ID NO: 419) AAACCCAAACTCCTAACTACC (SEQ ID NO: 420)	408
17	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	GTGGGGAGGTAGTTGAAGA (SEQ ID NO: 421) ATACACCCCTAACCCAAAAT (SEQ ID NO: 422)	478
18	CDKN2a (SEQ ID NO: 18)	TTGAAAATTAAGGGTTGAGG (SEQ ID NO: 423) CACCCTCTAATAACCAACCA (SEQ ID NO: 424)	598
19	CDKN2a (SEQ ID NO: 18)	GGGGTTGGTTGGTTATTAGA (SEQ ID NO: 425) AACCCTCTACCCACCTAAAT (SEQ ID NO: 426)	256
20	CDKN2B (SEQ ID NO: 19)	GGTTGGTTGAAGGAATAGAAAT (SEQ ID NO: 427) CCCACTAAACATACCCTTATTC (SEQ ID NO: 428)	708
21	CD44 (SEQ ID NO: 20)	GAAAGGAGAGGTTAAAGGTTG (SEQ ID NO: 429) AACTCACTTAACTCCAATCCC	696

No:	*Gene:*	*Primer:*	*Amplificate Length:*
		(SEQ ID NO: 430)	
22	CSPG2 (SEQ ID NO: 21)	GGATAGGAGTTGGGATTAAGAT (SEQ ID NO: 431) AAATCTTTTTCAACACCAAAAT (SEQ ID NO: 432)	414
23	DAPK1 (SEQ ID NO: 22)	AACCCTTTCTTCAAATTACAAA (SEQ ID NO: 433) TGATTGGGTTTTAGGGAAATA (SEQ ID NO: 434)	348
24	EGFR (SEQ ID NO: 23)	GGGTTTGGTTGTAATATGGATT (SEQ ID NO: 435) CCCAACACTACCCCTCTAA (SEQ ID NO: 436)	732
25	EYA4 (SEQ ID NO: 24)	GGAAGAGGTGATTAAATGGAT (SEQ ID NO: 437) CCCAAAAATCAAACAACAA (SEQ ID NO: 438)	226
26	GSTP1 (SEQ ID NO: 25)	ATTTGGGAAAGAGGGAAAG (SEQ ID NO: 439) TAAAAACTCTAAACCCCATCC (SEQ ID NO: 440)	300
27	GTBP/MSH6 (SEQ ID NO: 26)	CCCTACCCACCAATATACC (SEQ ID NO: 441) AGATTTGGGGAAGAAGTTGTA (SEQ ID NO: 442)	278
28	HIC-1 (SEQ ID NO: 27)	TGGGTTGGAGAAGAAGTTTA (SEQ ID NO: 443) TCATATTTCCAAAAACACACC (SEQ ID NO: 444)	280
29	HRAS (SEQ ID NO: 28)	CTTATTCCCATCTAAACCCTATT (SEQ ID NO: 445) GTGGTTTTGTGAAGTTTTAGGT (SEQ ID NO: 446)	331
30	IGF2 (SEQ ID NO: 29)	CCCTTCCCCTTAACTAAACT (SEQ ID NO: 447) AATTTGGGTTAGGTTTGGA (SEQ ID NO: 448)	364
31	LKB1 (SEQ ID NO: 30)	TAAAAGAAGGATTTTTGATTGG (SEQ ID NO: 449) CATCTTATTTACCTCCCTCCC (SEQ ID NO: 450)	528
32	MGMT (SEQ ID NO: 31)	AAGGTTTTAGGGAAGAGTGTTT (SEQ ID NO: 451) ACCTTTTCCTATCACAAAAATAA (SEQ ID NO: 452)	636
33	MLH1 (SEQ ID NO: 32)	TAAGGGGAGAGGAGGAGTTT (SEQ ID NO: 453) ACCAATTCTCAATCATCTCTTT (SEQ ID NO: 454)	545

No:	*Gene:*	*Primer:*	*Amplificate Length:*
34	MNCA9 (SEQ ID NO: 33)	GGGAAGTAGGTTAGGGTTAGTT (SEQ ID NO: 455) AAATCCTCCTCTCCAAATAAAT (SEQ ID NO: 456)	616
35	MSH3 (SEQ ID NO: 34)	TGTTTGGGATTGGGTAGG (SEQ ID NO: 457) CATAACCTTTACCTATCTCCTCA (SEQ ID NO: 458)	211
36	MYC (SEQ ID NO: 35)	AGAGGGAGTAAAAGAAAATGGT (SEQ ID NO: 459) CCAAATAAACAAAATAACCTCC (SEQ ID NO: 460)	712
37	N33 (SEQ ID NO: 36)	TTTTAGATTGAGGTTTTAGGGT (SEQ ID NO: 461) ATCCATTCTACCTCCTTTTTCT (SEQ ID NO: 462)	497
38	PAX6 (SEQ ID NO: 37)	GGAGGGGAGAGGGTTATG (SEQ ID NO: 463) TACTATACACACCCCAAAACAA (SEQ ID NO: 464)	374
39	PGR (SEQ ID NO: 38)	TTTTGGGAATGGGTTGTAT (SEQ ID NO: 465) CTACCCTTAACCTCCATCCTA (SEQ ID NO: 466)	369
40	PTEN (SEQ ID NO: 39)	TTTTAGGTAGTTATATTGGGTATGTT (SEQ ID NO: 467) TCAACTCTCAAACTTCCATCA (SEQ ID NO: 468)	346
41	RARB (SEQ ID NO: 40)	TTGTTGGGAGTTTTTAAGTTTT (SEQ ID NO: 469) CAAATTCTCCTTCCAAATAAAT (SEQ ID NO: 470)	353
42	SFN (SEQ ID NO: 41)	GAAGAGAGGAGAGGGAGGTA (SEQ ID NO: 471) CTATCCAACAAACCCAACA (SEQ ID NO: 472)	489
43	S100A2 (SEQ ID NO: 42)	GTTTTTAAGTTGGAGAAGAGGA (SEQ ID NO: 473) ACCTATAAATCACAACCCACTC (SEQ ID NO: 474)	460
44	TGFBR2 (SEQ ID NO: 43)	GTAATTTGAAGAAAGTTGAGGG (SEQ ID NO: 475) CCAACAACTAAACAAAACCTCT (SEQ ID NO: 476)	296
45	TIMP3 (SEQ ID NO: 44)	TGAGAAAATTGTTGTTTGAAGT (SEQ ID NO: 477) CAAAATACCCTAAAAACCACTC (SEQ ID NO: 478)	306
46	TP53	GGAGTTGTATTGTTGGGAGA	279

No:	*Gene:*	*Primer:*	*Amplificate Length:*
	(SEQ ID NO: 45)	(SEQ ID NO: 479) TAAAACCCCAATTTTCACTAA (SEQ ID NO: 480)	
47	TP73 (SEQ ID NO: 46)	AGTAAATAGTGGGTGAGTTATGAA (SEQ ID NO: 481) GAAAAACCTCTAAAAACTACTCTCC (SEQ ID NO: 482)	607
48	VHL (SEQ ID NO: 47)	TGTAAAATGAATAAAGTTAATGAGTG (SEQ ID NO: 483) TCCTAAATTCAAATAATCCTCCT (SEQ ID NO: 484)	362
49	CDKN1C (SEQ ID NO: 48)	GGGGAGGTAGATATTTGGATAA (SEQ ID NO: 485) AACTACACCATTTATATTCCCAC (SEQ ID NO: 486)	300
50	CAV1 (SEQ ID NO: 49)	GTTAGTATGTTTGGGGGTAAAT (SEQ ID NO: 487) ATAAATAACACCTTCCACCCTA (SEQ ID NO: 488)	435
51	CDH13 (SEQ ID NO: 50)	TTTGTATTAGGTTGGAAGTGGT (SEQ ID NO: 489) CCCAAATAAATCAACAACAACA (SEQ ID NO: 490)	286
52	DRG1 (SEQ ID NO: 51)	GGTTTTGGGTTTAGTGGTAAAT (SEQ ID NO: 491) AACTTTCATAACTCACCCTTTC (SEQ ID NO: 492)	416
53	PTGS2 (SEQ ID NO: 52)	GATTTTTGGAGAGGAAGTTAAG (SEQ ID NO: 493) AAAACTAAAAACCAAACCCATA (SEQ ID NO: 494)	381
54	THBS1 (SEQ ID NO: 53)	TGGGGTTAGTTTAGGATAGG (SEQ ID NO: 495) CTTAAAAACACTAAAACTTCTCAAA (SEQ ID NO: 496)	398
55	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	TTGTTTGGGTTAATAAATGGA (SEQ ID NO: 497) CTTCTCTCTTCTCCCCTCTC (SEQ ID NO: 498)	295
56	DNMT1 (SEQ ID NO: 55)	TCCCCATCACACCTAAAA (SEQ ID NO: 499) GGGAGGAGGGGATGTATT (SEQ ID NO: 500)	210
57	CEA (SEQ ID NO: 56)	TATGGGAGGAGGTTAGTAAGTG (SEQ ID NO: 501) CCCCAAATCCTACATATAAAAA (SEQ ID NO: 502)	680
58	MB (SEQ ID NO: 57)	GTTTTTGGTAAAGGGGTAGAA (SEQ ID NO: 503)	598

No:	*Gene:*	*Primer:*	*Amplificate Length:*
		CCTAAAATATCAACCTCCACCT (SEQ ID NO: 504)	
59	PCNA (SEQ ID NO: 58)	TTTTTAGGTTGTAAGGAGGTTTT (SEQ ID NO: 505) TAAATACCTCCAACACCTTTCT (SEQ ID NO: 506)	608
60	CDC2 (SEQ ID NO: 59)	ATTAGAAGTGAAAGTAATGGAATTT (SEQ ID NO: 507) TCAATTTCCAAAAACCAAC (SEQ ID NO: 508)	418
61	ESR1 (SEQ ID NO: 60)	AGGGGGAATTAAATAGAAAGAG (SEQ ID NO: 509) CAATAAAACCATCCCAAATACT (SEQ ID NO: 510)	662
62	CASP8 (SEQ ID NO: 61)	AGTGGATTTGGAGTTTAGATGT (SEQ ID NO: 511) AACAAAATAAAAACTTCTCCCA (SEQ ID NO: 512)	431
63	RASSF1 (SEQ ID NO: 62)	ACCTCTCTACAAATTACAAATTCA (SEQ ID NO: 513) AGTTTGGGTTAGTTTGGGTT (SEQ ID NO: 514)	347
64	MSH4 (SEQ ID NO: 63)	AGGATGTTGAGGTTTGAGATT (SEQ ID NO: 515) CACTATAATAACCACCACCCA (SEQ ID NO: 516)	339
65	MSH5 (SEQ ID NO: 64)	TATTAGGAATAAAGTTGGGGAG (SEQ ID NO: 517) AACCCTTCAAACAAAAATAAAA (SEQ ID NO: 518)	395

Table 2: Hybridisation oligonucleotides

No:	*Gene*	*Oligo:*
1	MDR1 (SEQ ID NO: 1)	TTGGTGGTCGTTTTAAGG (SEQ ID NO: 519)
2	MDR1 (SEQ ID NO: 1)	TTGGTGGTTGTTTTAAGG (SEQ ID NO: 520)
3	MDR1 (SEQ ID NO: 1)	TTGAAAGACGTGTTTATA (SEQ ID NO: 521)
4	MDR1 (SEQ ID NO: 1)	TTGAAAGATGTGTTTATA (SEQ ID NO: 522)
5	MDR1 (SEQ ID NO: 1)	AGGTGTAACGGAAGTTAG (SEQ ID NO: 523)
6	MDR1 (SEQ ID NO: 1)	AGGTGTAATGGAAGTTAG (SEQ ID NO: 524)
7	MDR1 (SEQ ID NO: 1)	TAGTTTTTCGAGGAATTA (SEQ ID NO: 525)
8	MDR1	TAGTTTTTTGAGGAATTA

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 1)	(SEQ ID NO: 526)
9	APOC2 (SEQ ID NO: 2)	GAGAGTTTCGTTTTTGTT (SEQ ID NO: 527)
10	APOC2 (SEQ ID NO: 2)	GAGAGTTTTGTTTTTGTT (SEQ ID NO: 528)
11	APOC2 (SEQ ID NO: 2)	TTGGGGGACGTTATTGTT (SEQ ID NO: 529)
12	APOC2 (SEQ ID NO: 2)	TTGGGGGATGTTATTGTT (SEQ ID NO: 530)
13	APOC2 (SEQ ID NO: 2)	TGTGTTCGTTCGGAGTTG (SEQ ID NO: 531)
14	APOC2 (SEQ ID NO: 2)	TGTGTTTGTTTGGAGTTG (SEQ ID NO: 532)
15	APOC2 (SEQ ID NO: 2)	TGGGTTTGCGGAGAATGG (SEQ ID NO: 533)
16	APOC2 (SEQ ID NO: 2)	TGGGTTTGTGGAGAATGG (SEQ ID NO: 534)
17	CACNA1G (SEQ ID NO: 3)	TTTAGGAGCGTTAATGTG (SEQ ID NO: 535)
18	CACNA1G (SEQ ID NO: 3)	TTTAGGAGTGTTAATGTG (SEQ ID NO: 536)
19	CACNA1G (SEQ ID NO: 3)	TAGGGTTACGAGGTTAGG (SEQ ID NO: 537)
20	CACNA1G (SEQ ID NO: 3)	TAGGGTTATGAGGTTAGG (SEQ ID NO: 538)
21	CACNA1G (SEQ ID NO: 3)	GGAGGTTACGTTTAGATT (SEQ ID NO: 539)
22	CACNA1G (SEQ ID NO: 3)	GGAGGTTATGTTTAGATT (SEQ ID NO: 540)
23	CACNA1G (SEQ ID NO: 3)	TTAGGGGTCGTGGATAAA (SEQ ID NO: 541)
24	CACNA1G (SEQ ID NO: 3)	TTAGGGGTTGTGGATAAA (SEQ ID NO: 542)
25	EGR4 (SEQ ID NO: 4)	GGTGGGAAGCGTATTTAT (SEQ ID NO: 543)
26	EGR4 (SEQ ID NO: 4)	GGTGGGAAGTGTATTTAT (SEQ ID NO: 544)
27	EGR4 (SEQ ID NO: 4)	TTATAGTTCGAGTTTTTT (SEQ ID NO: 545)
28	EGR4 (SEQ ID NO: 4)	TTATAGTTTGAGTTTTTT (SEQ ID NO: 546)
29	EGR4 (SEQ ID NO: 4)	GGAGTTTTCGGTATATAT (SEQ ID NO: 927)
30	EGR4 (SEQ ID NO: 4)	GGAGTTTTTGGTATATAT (SEQ ID NO: 928)
31	AR (SEQ ID NO: 5)	TGTTATTTCGAGAGAGGT (SEQ ID NO: 547)
32	AR (SEQ ID NO: 5)	TGTTATTTTGAGAGAGGT (SEQ ID NO: 548)
33	AR	AGAGGTTGCGTTTTAGAG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 5)	(SEQ ID NO: 1027)
34	AR (SEQ ID NO: 5)	AGAGGTTGTGTTTTAGAG (SEQ ID NO: 1028)
35	AR (SEQ ID NO: 5)	ATTTTGAGCGAGGTTAGT (SEQ ID NO: 549)
36	AR (SEQ ID NO: 5)	ATTTTGAGTGAGGTTAGT (SEQ ID NO: 550)
37	AR (SEQ ID NO: 5)	GTAGTATTCGAAGGTAGT (SEQ ID NO: 551)
38	AR (SEQ ID NO: 5)	GTAGTATTTGAAGGTAGT (SEQ ID NO: 552)
39	RB1 (SEQ ID NO: 6)	TTAGATTTCGGGATAGGG (SEQ ID NO: 553)
40	RB1 (SEQ ID NO: 6)	TTAGATTTTGGGATAGGG (SEQ ID NO: 554)
41	RB1 (SEQ ID NO: 6)	TATAGTTTCGTTAAGTGT (SEQ ID NO: 555)
42	RB1 (SEQ ID NO: 6)	TATAGTTTTGTTAAGTGT (SEQ ID NO: 556)
43	RB1 (SEQ ID NO: 6)	GTGTATTTCGGTTTGGAG (SEQ ID NO: 557)
44	RB1 (SEQ ID NO: 6)	GTGTATTTTGGTTTGGAG (SEQ ID NO: 558)
45	RB1 (SEQ ID NO: 6)	TGGATTTACGTTAGGTTT (SEQ ID NO: 559)
46	RB1 (SEQ ID NO: 6)	TGGATTTATGTTAGGTTT (SEQ ID NO: 560)
47	GPIb beta (SEQ ID NO: 7)	TGTTATTTGTCGTTGTAG (SEQ ID NO: 561)
48	GPIb beta (SEQ ID NO: 7)	TGTTATTTGTTGTTGTAG (SEQ ID NO: 562)
49	GPIb beta (SEQ ID NO: 7)	GTGGGAGCGGAAGTTTGA (SEQ ID NO: 563)
50	GPIb beta (SEQ ID NO: 7)	GTGGGAGTGGAAGTTTGA (SEQ ID NO: 564)
51	GPIb beta (SEQ ID NO: 7)	TAGAGTAAGTCGGGTTGT (SEQ ID NO: 565)
52	GPIb beta (SEQ ID NO: 7)	TAGAGTAAGTCGGGTTGTT (SEQ ID NO: 566)
53	GPIb beta (SEQ ID NO: 7)	GGTTAGGTCGTAGTATTG (SEQ ID NO: 567)
54	GPIb beta (SEQ ID NO: 7)	GGTTAGGTTGTAGTATTG (SEQ ID NO: 568)
55	GPIb beta (SEQ ID NO: 7)	GGAGTTCGGTCGGGTTTT (SEQ ID NO: 1005)
56	GPIb beta (SEQ ID NO: 7)	GGAGTTTGGTTGGGTTTT (SEQ ID NO: 1006)
57	MYOD1 (SEQ ID NO: 8)	ATAGTAGTCGGGTGTTGG (SEQ ID NO: 569)
58	MYOD1	ATAGTAGTTGGGTGTTGG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 8)	(SEQ ID NO: 570)
59	MYOD1 (SEQ ID NO: 8)	GTGTTAGTCGTTTAGGGT (SEQ ID NO: 1009)
60	MYOD1 (SEQ ID NO: 8)	GTGTTAGTTGTTTAGGGT (SEQ ID NO: 1010)
61	MYOD1 (SEQ ID NO: 8)	TAGTTGTTCGTTTGGGTT (SEQ ID NO: 571)
62	MYOD1 (SEQ ID NO: 8)	TAGTTGTTTGTTTGGGTT (SEQ ID NO: 572)
63	MYOD1 (SEQ ID NO: 8)	AATTAGGTCGGATAGGAG (SEQ ID NO: 975)
64	MYOD1 (SEQ ID NO: 8)	AATTAGGTTGGATAGGAG (SEQ ID NO: 976)
65	WT1 (SEQ ID NO: 9)	TAGTGAGACGAGGTTTTT (SEQ ID NO: 1017)
66	WT1 (SEQ ID NO: 9)	TAGTGAGATGAGGTTTTT (SEQ ID NO: 1018)
67	WT1 (SEQ ID NO: 9)	TATATTGGCGAAGGTTAA (SEQ ID NO: 967)
68	WT1 (SEQ ID NO: 9)	TATATTGGTGAAGGTTAA (SEQ ID NO: 968)
69	WT1 (SEQ ID NO: 9)	TGTTATATCGGTTAGTTG (SEQ ID NO: 959)
70	WT1 (SEQ ID NO: 9)	TGTTATATTGGTTAGTTG (SEQ ID NO: 960)
71	WT1 (SEQ ID NO: 9)	TTTAGTTTCGATTTTTGG (SEQ ID NO: 573)
72	WT1 (SEQ ID NO: 9)	TTTAGTTTTGATTTTTGG (SEQ ID NO: 574)
73	HLA-F (SEQ ID NO: 10)	ATAGGGTACGTTAAGGTT (SEQ ID NO: 575)
74	HLA-F (SEQ ID NO: 10)	ATAGGGTATGTTAAGGTT (SEQ ID NO: 576)
75	HLA-F (SEQ ID NO: 10)	TATTTGGGCGGGTGAGTG (SEQ ID NO: 939)
76	HLA-F (SEQ ID NO: 10)	TATTTGGGTGGGTGAGTG (SEQ ID NO: 940)
77	HLA-F (SEQ ID NO: 10)	GAGAGAAACGGTTTTTGT (SEQ ID NO: 577)
78	HLA-F (SEQ ID NO: 10)	GAGAGAAATGGTTTTTGT (SEQ ID NO: 578)
79	HLA-F (SEQ ID NO: 10)	AGTTGTTTCGTAGATATT (SEQ ID NO: 989)
80	HLA-F (SEQ ID NO: 10)	AGTTGTTTTGTAGATATT (SEQ ID NO: 990)
81	ELK1 (SEQ ID NO: 11)	TGTTTAATCGTAGAGTTG (SEQ ID NO: 579)
82	ELK1 (SEQ ID NO: 11)	TGTTTAATTGTAGAGTTG (SEQ ID NO: 580)
83	ELK1	TTTGTTTTCGTTGAGTAG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 11)	(SEQ ID NO: 581)
84	ELK1 (SEQ ID NO: 11)	TTTGTTTTTGTTGAGTAG (SEQ ID NO: 582)
85	ELK1 (SEQ ID NO: 11)	GAAGGGTTCGTTTTTTAA (SEQ ID NO: 583)
86	ELK1 (SEQ ID NO: 11)	GAAGGGTTTGTTTTTTAA (SEQ ID NO: 584)
87	ELK1 (SEQ ID NO: 11)	ATTAATAGCGTTTTGGTT (SEQ ID NO: 585)
88	ELK1 (SEQ ID NO: 11)	ATTAATAGTGTTTTGGTT (SEQ ID NO: 586)
89	APC (SEQ ID NO: 12)	TTTAATCGTATAGTTTGT (SEQ ID NO: 971)
90	APC (SEQ ID NO: 12)	TTTAATTGTATAGTTTGT (SEQ ID NO: 972)
91	APC (SEQ ID NO: 12)	TATTTAGCGGATTATATA (SEQ ID NO: 587)
92	APC (SEQ ID NO: 12)	TATTTAGTGGATTATATA (SEQ ID NO: 588)
93	APC (SEQ ID NO: 12)	TATTTTGGCGGGTTGTAT (SEQ ID NO: 985)
94	APC (SEQ ID NO: 12)	TATTTTGGTGGGTTGTAT (SEQ ID NO: 986)
95	APC (SEQ ID NO: 12)	AAGGTTATCGGTTTAAGA (SEQ ID NO: 589)
96	APC (SEQ ID NO: 12)	AAGGTTATTGGTTTAAGA (SEQ ID NO: 590)
97	APC (SEQ ID NO: 12)	GGGGGACGACGTTTTTGT (SEQ ID NO: 591)
98	APC (SEQ ID NO: 12)	GGGGGATGATGTTTTTGT (SEQ ID NO: 592)
99	BCL2 (SEQ ID NO: 13)	AGTGTTTCGCGTGATTGA (SEQ ID NO: 593)
100	BCL2 (SEQ ID NO: 13)	AGTGTTTTGTGTGATTGA (SEQ ID NO: 594)
101	BCL2 (SEQ ID NO: 13)	TAAGTTGTCGTAGAGGGG (SEQ ID NO: 595)
102	BCL2 (SEQ ID NO: 13)	TAAGTTGTTGTAGAGGGG (SEQ ID NO: 596)
103	BCL2 (SEQ ID NO: 13)	GGATTTCGTCGTTGTAGA (SEQ ID NO: 597)
104	BCL2 (SEQ ID NO: 13)	GGATTTTGTTGTTGTAGA (SEQ ID NO: 598)
105	BCL2 (SEQ ID NO: 13)	TTTTGTTACGGTGGTGGA (SEQ ID NO: 1025)
106	BCL2 (SEQ ID NO: 13)	TTTTGTTATGGTGGTGGA (SEQ ID NO: 1026)
107	CALCA (SEQ ID NO: 14)	GAGGGTGACGTAATTTAG (SEQ ID NO: 599)
108	CALCA	GAGGGTGATGTAATTTAG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 14)	(SEQ ID NO: 600)
109	CALCA (SEQ ID NO: 14)	TGTATTGGCGGAATTTTT (SEQ ID NO: 601)
110	CALCA (SEQ ID NO: 14)	TGTATTGGTGGAATTTTT (SEQ ID NO: 602)
111	CALCA (SEQ ID NO: 14)	ATTAGGTTCGTGTTTTAG (SEQ ID NO: 953)
112	CALCA (SEQ ID NO: 14)	ATTAGGTTTGTGTTTTAG (SEQ ID NO: 954)
113	CALCA (SEQ ID NO: 14)	GTTAGTTTCGGGATATTT (SEQ ID NO: 603)
114	CALCA (SEQ ID NO: 14)	GTTAGTTTTGGGATATTT (SEQ ID NO: 604)
115	CDH1 (SEQ ID NO: 15)	TAGAGGATCGTTTGAGTT (SEQ ID NO: 605)
116	CDH1 (SEQ ID NO: 15)	TAGAGGATTGTTTGAGTT (SEQ ID NO: 606)
117	CDH1 (SEQ ID NO: 15)	GTTGTGATCGTATTATTG (SEQ ID NO: 607)
118	CDH1 (SEQ ID NO: 15)	GTTGTGATTGTATTATTG (SEQ ID NO: 608)
119	CDH1 (SEQ ID NO: 15)	TTGGGATTCGAATTTAGT (SEQ ID NO: 609)
120	CDH1 (SEQ ID NO: 15)	TTGGGATTTGAATTTAGT (SEQ ID NO: 610)
121	CDH1 (SEQ ID NO: 15)	AGGGTTATCGCGTTTATG (SEQ ID NO: 983)
122	CDH1 (SEQ ID NO: 15)	AGGGTTATTGTGTTTATG (SEQ ID NO: 984)
123	CDH1 (SEQ ID NO: 15)	TAGTGGCGTCGGAATTGT (SEQ ID NO: 929)
124	CDH1 (SEQ ID NO: 15)	TAGTGGTGTTGGAATTGT (SEQ ID NO: 930)
125	CDKN1A (SEQ ID NO: 16)	AGGTGTATCGTTTTTATA (SEQ ID NO: 611)
126	CDKN1A (SEQ ID NO: 16)	AGGTGTATTGTTTTTATA (SEQ ID NO: 612)
127	CDKN1A (SEQ ID NO: 16)	TGGGTTAGCGGTGAGTTA (SEQ ID NO: 613)
128	CDKN1A (SEQ ID NO: 16)	TGGGTTAGTGGTGAGTTA (SEQ ID NO: 614)
129	CDKN1A (SEQ ID NO: 16)	GTTTATTTCGTGGGGAAA (SEQ ID NO: 615)
130	CDKN1A (SEQ ID NO: 16)	GTTTATTTTGTGGGGAAA (SEQ ID NO: 616)
131	CDKN1A (SEQ ID NO: 16)	TTGGAATTCGGTTAGGTT (SEQ ID NO: 617)
132	CDKN1A (SEQ ID NO: 16)	TTGGAATTTGGTTAGGTT (SEQ ID NO: 618)
133	CDKN1B (p27	AAGAGAAACGTTGGAATA

No:	*Gene*	*Oligo:*
	Kip1) (SEQ ID NO: 17)	(SEQ ID NO: 619)
134	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	AAGAGAAATGTTGGAATA (SEQ ID NO: 620)
135	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	TTTGATTTCGAGGGGAGT (SEQ ID NO: 621)
136	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	TTTGATTTTGAGGGGAGT (SEQ ID NO: 622)
137	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	GTATTTGGCGGTTGGATT (SEQ ID NO: 623)
138	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	GTATTTGGTGGTTGGATT (SEQ ID NO: 624)
139	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	TATAATTTCGGGAAAGAA (SEQ ID NO: 625)
140	CDKN1B (p27 Kip1) (SEQ ID NO: 17)	TATAATTTTGGGAAAGAA (SEQ ID NO: 626)
141	CDKN2a (SEQ ID NO: 18)	AGAGTGAACGTATTTAAA (SEQ ID NO: 627)
142	CDKN2a (SEQ ID NO: 18)	AGAGTGAATGTATTTAAA (SEQ ID NO: 628)
143	CDKN2a (SEQ ID NO: 18)	GTTGTTTTCGGTTGGTGT (SEQ ID NO: 1029)
144	CDKN2a (SEQ ID NO: 18)	GTTGTTTTTGGTTGGTGT (SEQ ID NO: 1030)
145	CDKN2a (SEQ ID NO: 18)	GATAGGGTCGGAGGGGGT (SEQ ID NO: 629)
146	CDKN2a (SEQ ID NO: 18)	GATAGGGTTGGAGGGGGT (SEQ ID NO: 630)
147	CDKN2a (SEQ ID NO: 18)	GGAGTTTTCGGTTGATTG (SEQ ID NO: 997)
148	CDKN2a (SEQ ID NO: 18)	GGAGTTTTTGGTTGATTG (SEQ ID NO: 998)
149	CDKN2a (SEQ ID NO: 18)	AATAGTTACGGTCGGAGG (SEQ ID NO: 981)
150	CDKN2a (SEQ ID NO: 18)	AATAGTTATGGTTGGAGG (SEQ ID NO: 982)
151	CDKN2B (SEQ ID NO: 19)	ATATTTAGCGAGTAGTGT (SEQ ID NO: 631)
152	CDKN2B (SEQ ID NO: 19)	ATATTTAGTGAGTAGTGT (SEQ ID NO: 632)
153	CDKN2B (SEQ ID NO: 19)	ATAGGGGGCGGAGTTTAA (SEQ ID NO: 633)
154	CDKN2B	ATAGGGGGTGGAGTTTAA

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 19)	(SEQ ID NO: 634)
155	CDKN2B (SEQ ID NO: 19)	TTATTGTACGGGGTTTTA (SEQ ID NO: 635)
156	CDKN2B (SEQ ID NO: 19)	TTATTGTATGGGGTTTTA (SEQ ID NO: 636)
157	CDKN2B (SEQ ID NO: 19)	TTTTAAGTCGTAGAAGGA (SEQ ID NO: 637)
158	CDKN2B (SEQ ID NO: 19)	TTTTAAGTTGTAGAAGGA (SEQ ID NO: 638)
159	CD44 (SEQ ID NO: 20)	GTGGGGTTCGGAGGTATA (SEQ ID NO: 919)
160	CD44 (SEQ ID NO: 20)	GTGGGGTTTGGAGGTATA (SEQ ID NO: 920)
161	CD44 (SEQ ID NO: 20)	GGTAGTTTCGATTATTTA (SEQ ID NO: 639)
162	CD44 (SEQ ID NO: 20)	GGTAGTTTTGATTATTTA (SEQ ID NO: 640)
163	CD44 (SEQ ID NO: 20)	TTGTTTAGCGGATTTTAG (SEQ ID NO: 897)
164	CD44 (SEQ ID NO: 20)	TTGTTTAGTGGATTTTAG (SEQ ID NO: 898)
165	CD44 (SEQ ID NO: 20)	TGGTGGTACGTAGTTTGG (SEQ ID NO: 641)
166	CD44 (SEQ ID NO: 20)	TGGTGGTATGTAGTTTGG (SEQ ID NO: 642)
167	CSPG2 (SEQ ID NO: 21)	AAGATTTTCGGTTAGTTT (SEQ ID NO: 963)
168	CSPG2 (SEQ ID NO: 21)	AAGATTTTTGGTTAGTTT (SEQ ID NO: 964)
169	CSPG2 (SEQ ID NO: 21)	ATGTGATTCGTTTGGGTA (SEQ ID NO: 643)
170	CSPG2 (SEQ ID NO: 21)	ATGTGATTTGTTTGGGTA (SEQ ID NO: 644)
171	CSPG2 (SEQ ID NO: 21)	GGGTAACGTCGAATTTAG (SEQ ID NO: 901)
172	CSPG2 (SEQ ID NO: 21)	GGGTAATGTTGAATTTAG (SEQ ID NO: 902)
173	CSPG2 (SEQ ID NO: 21)	AAAAATTCGCGAGTTTAG (SEQ ID NO: 945)
174	CSPG2 (SEQ ID NO: 21)	AAAAATTTGTGAGTTTAG (SEQ ID NO: 946)
175	DAPK1 (SEQ ID NO: 22)	GTTGGAGTCGAGGTTTGA (SEQ ID NO: 645)
176	DAPK1 (SEQ ID NO: 22)	GTTGGAGTTGAGGTTTGA (SEQ ID NO: 646)
177	DAPK1 (SEQ ID NO: 22)	TTTTTTGTCGGATTGGTG (SEQ ID NO: 647)
178	DAPK1 (SEQ ID NO: 22)	TTTTTTGTTGGATTGGTG (SEQ ID NO: 648)
179	DAPK1	GAAGGGAGCGTATTTTAT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 22)	(SEQ ID NO: 955)
180	DAPK1 (SEQ ID NO: 22)	GAAGGGAGTGTATTTTAT (SEQ ID NO: 956)
181	DAPK1 (SEQ ID NO: 22)	TTGTTTTTCGGAAATTTG (SEQ ID NO: 935)
182	DAPK1 (SEQ ID NO: 22)	TTGTTTTTTGGAAATTTG (SEQ ID NO: 936)
183	EGFR (SEQ ID NO: 23)	TTTGTATTCGGAGTTGGG (SEQ ID NO: 961)
184	EGFR (SEQ ID NO: 23)	TTTGTATTTGGAGTTGGG (SEQ ID NO: 962)
185	EGFR (SEQ ID NO: 23)	GATGATTTCGAGGGTGTT (SEQ ID NO: 649)
186	EGFR (SEQ ID NO: 23)	GATGATTTTGAGGGTGTT (SEQ ID NO: 650)
187	EGFR (SEQ ID NO: 23)	GAGGGTTTCGTAGTGTTG (SEQ ID NO: 651)
188	EGFR (SEQ ID NO: 23)	GAGGGTTTTGTAGTGTTG (SEQ ID NO: 652)
189	EGFR (SEQ ID NO: 23)	TGGGGATTCGAATAAAGG (SEQ ID NO: 653)
190	EGFR (SEQ ID NO: 23)	TGGGGATTTGAATAAAGG (SEQ ID NO: 654)
191	EGFR (SEQ ID NO: 23)	ATTTGGTTCGATTTGGAT (SEQ ID NO: 931)
192	EGFR (SEQ ID NO: 23)	ATTTGGTTTGATTTGGAT (SEQ ID NO: 932)
193	EYA4 (SEQ ID NO: 24)	TATATATACGTGTGGGTA (SEQ ID NO: 655)
194	EYA4 (SEQ ID NO: 24)	TATATATATGTGTGGGTA (SEQ ID NO: 656)
195	EYA4 (SEQ ID NO: 24)	AGTGTATGCGTAGAAGGT (SEQ ID NO: 923)
196	EYA4 (SEQ ID NO: 24)	AGTGTATGTGTAGAAGGT (SEQ ID NO: 924)
197	EYA4 (SEQ ID NO: 24)	TTTAGATACGAAATGTTA (SEQ ID NO: 657)
198	EYA4 (SEQ ID NO: 24)	TTTAGATATGAAATGTTA (SEQ ID NO: 658)
199	EYA4 (SEQ ID NO: 24)	AAGTAAGTCGTTGTTGTT (SEQ ID NO: 921)
200	EYA4 (SEQ ID NO: 24)	AAGTAAGTTGTTGTTGTT (SEQ ID NO: 922)
201	GSTP1 (SEQ ID NO: 25)	GGTTTTTTCGGTTAGTTG (SEQ ID NO: 659)
202	GSTP1 (SEQ ID NO: 25)	GGTTTTTTTGGTTAGTTG (SEQ ID NO: 660)
203	GSTP1 (SEQ ID NO: 25)	GGAGTTCGCGGGATTTTT (SEQ ID NO: 905)
204	GSTP1	GGAGTTTGTGGGATTTTT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 25)	(SEQ ID NO: 906)
205	GSTP1 (SEQ ID NO: 25)	GTAGTTTTCGTTATTAGT (SEQ ID NO: 661)
206	GSTP1 (SEQ ID NO: 25)	GTAGTTTTTGTTATTAGT (SEQ ID NO: 662)
207	GTBP/MSH6 (SEQ ID NO: 26)	GAGGAATTCGGGTTTTAG (SEQ ID NO: 951)
208	GTBP/MSH6 (SEQ ID NO: 26)	GAGGAATTTGGGTTTTAG (SEQ ID NO: 952)
209	GTBP/MSH6 (SEQ ID NO: 26)	TTTGTTGGCGGGAAATTT (SEQ ID NO: 925)
210	GTBP/MSH6 (SEQ ID NO: 26)	TTTGTTGGTGGGAAATTT (SEQ ID NO: 926)
211	GTBP/MSH6 (SEQ ID NO: 26)	TTTTGTCGGACGGAGTTT (SEQ ID NO: 663)
212	GTBP/MSH6 (SEQ ID NO: 26)	TTTTGTTGGATGGAGTTT (SEQ ID NO: 664)
213	GTBP/MSH6 (SEQ ID NO: 26)	AAGGTTTAATCGTTTTGT (SEQ ID NO: 665)
214	GTBP/MSH6 (SEQ ID NO: 26)	AAGGTTTAATTGTTTTGT (SEQ ID NO: 666)
215	HIC-1 (SEQ ID NO: 27)	TTAAAACGGCGTATAGGG (SEQ ID NO: 667)
216	HIC-1 (SEQ ID NO: 27)	TTAAAATGGTGTATAGGG (SEQ ID NO: 668)
217	HIC-1 (SEQ ID NO: 27)	AGGAGATTCGAAAGTTTA (SEQ ID NO: 669)
218	HIC-1 (SEQ ID NO: 27)	AGGAGATTTGAAAGTTTA (SEQ ID NO: 670)
219	HIC-1 (SEQ ID NO: 27)	TTTTAGAGCGTTAGGGTT (SEQ ID NO: 1021)
220	HIC-1 (SEQ ID NO: 27)	TTTTAGAGTGTTAGGGTT (SEQ ID NO: 1022)
221	HRAS (SEQ ID NO: 28)	ATAGTGGGCGTAATTGGT (SEQ ID NO: 671)
222	HRAS (SEQ ID NO: 28)	ATAGTGGGTGTAATTGGT (SEQ ID NO: 672)
223	HRAS (SEQ ID NO: 28)	AAATTGGACGTTTAGTTG (SEQ ID NO: 673)
224	HRAS (SEQ ID NO: 28)	AAATTGGATGTTTAGTTG (SEQ ID NO: 674)
225	HRAS (SEQ ID NO: 28)	TAGAAGTCGAGAGATTTG (SEQ ID NO: 675)
226	HRAS (SEQ ID NO: 28)	TAGAAGTTGAGAGATTTG (SEQ ID NO: 676)
227	HRAS (SEQ ID NO: 28)	GAATATTTCGAAGTTTGT (SEQ ID NO: 677)
228	HRAS (SEQ ID NO: 28)	GAATATTTTGAAGTTTGT (SEQ ID NO: 678)
229	IGF2	AGTTTGAACGATGTAAGA

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 29)	(SEQ ID NO: 973)
230	IGF2 (SEQ ID NO: 29)	AGTTTGAATGATGTAAGA (SEQ ID NO: 974)
231	IGF2 (SEQ ID NO: 29)	GGTTATTACGATAATTTG (SEQ ID NO: 679)
232	IGF2 (SEQ ID NO: 29)	GGTTATTATGATAATTTG (SEQ ID NO: 680)
233	IGF2 (SEQ ID NO: 29)	TTGTATGGTCGAGTTTAT (SEQ ID NO: 941)
234	IGF2 (SEQ ID NO: 29)	TTGTATGGTTGAGTTTAT (SEQ ID NO: 942)
235	IGF2 (SEQ ID NO: 29)	GATTAGGGCGGGAAATAT (SEQ ID NO: 937)
236	IGF2 (SEQ ID NO: 29)	GATTAGGGTGGGAAATAT (SEQ ID NO: 938)
237	IGF2 (SEQ ID NO: 29)	TGGAGTTTACGGAGGTTT (SEQ ID NO: 681)
238	IGF2 (SEQ ID NO: 29)	TGGAGTTTATGGAGGTTT (SEQ ID NO: 682)
239	LKB1 (SEQ ID NO: 30)	TTAATTAACGGGTGGGTA (SEQ ID NO: 683)
240	LKB1 (SEQ ID NO: 30)	TTAATTAATGGGTGGGTA (SEQ ID NO: 684)
241	LKB1 (SEQ ID NO: 30)	TTTAGGTTCGTAAGTTTA (SEQ ID NO: 965)
242	LKB1 (SEQ ID NO: 30)	TTTAGGTTTGTAAGTTTA (SEQ ID NO: 966)
243	LKB1 (SEQ ID NO: 30)	AGGGAGGTCGTTGGTATT (SEQ ID NO: 933)
244	LKB1 (SEQ ID NO: 30)	AGGGAGGTTGTTGGTATT (SEQ ID NO: 934)
245	MGMT (SEQ ID NO: 31)	TAAGGATACGAGTTATAT (SEQ ID NO: 685)
246	MGMT (SEQ ID NO: 31)	TAAGGATATGAGTTATAT (SEQ ID NO: 686)
247	MGMT (SEQ ID NO: 31)	TTGGAGAGCGGTTGAGTT (SEQ ID NO: 687)
248	MGMT (SEQ ID NO: 31)	TTGGAGAGTGGTTGAGTT (SEQ ID NO: 688)
249	MGMT (SEQ ID NO: 31)	TAGGTTATCGGTGATTGT (SEQ ID NO: 689)
250	MGMT (SEQ ID NO: 31)	TAGGTTATTGGTGATTGT (SEQ ID NO: 690)
251	MGMT (SEQ ID NO: 31)	TAGGGGAGCGGTTTTAGG (SEQ ID NO: 691)
252	MGMT (SEQ ID NO: 31)	TAGGGGAGTGGTTTTAGG (SEQ ID NO: 692)
253	MGMT (SEQ ID NO: 31)	AGTAGGATCGGGATTTTT (SEQ ID NO: 1001)
254	MGMT	AGTAGGATTGGGATTTTT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 31)	(SEQ ID NO: 1002)
255	MLH1 (SEQ ID NO: 32)	TTGAGAAGCGTTAAGTAT (SEQ ID NO: 693)
256	MLH1 (SEQ ID NO: 32)	TTGAGAAGTGTTAAGTAT (SEQ ID NO: 694)
257	MLH1 (SEQ ID NO: 32)	TTAGGTAGCGGGTAGTAG (SEQ ID NO: 949)
258	MLH1 (SEQ ID NO: 32)	TTAGGTAGTGGGTAGTAG (SEQ ID NO: 950)
259	MLH1 (SEQ ID NO: 32)	GTAGTAGTCGTTTTAGGG (SEQ ID NO: 695)
260	MLH1 (SEQ ID NO: 32)	GTAGTAGTTGTTTTAGGG (SEQ ID NO: 696)
261	MLH1 (SEQ ID NO: 32)	ATAGTTGTCGTTGAAGGG (SEQ ID NO: 697)
262	MLH1 (SEQ ID NO: 32)	ATAGTTGTTGTTGAAGGG (SEQ ID NO: 698)
263	MLH1 (SEQ ID NO: 32)	TTGGATGGCGTAAGTTAT (SEQ ID NO: 699)
264	MLH1 (SEQ ID NO: 32)	TTGGATGGTGTAAGTTAT (SEQ ID NO: 700)
265	MNCA9 (SEQ ID NO: 33)	TAAAAGGGCGTTTTGTGA (SEQ ID NO: 701)
266	MNCA9 (SEQ ID NO: 33)	TAAAAGGGTGTTTTGTGA (SEQ ID NO: 702)
267	MNCA9 (SEQ ID NO: 33)	TAGTTAGTCGTATGGTTT (SEQ ID NO: 703)
268	MNCA9 (SEQ ID NO: 33)	TAGTTAGTTGTATGGTTT (SEQ ID NO: 704)
269	MNCA9 (SEQ ID NO: 33)	GATTTATTCGGAGAGGAG (SEQ ID NO: 705)
270	MNCA9 (SEQ ID NO: 33)	GATTTATTTGGAGAGGAG (SEQ ID NO: 706)
271	MSH3 (SEQ ID NO: 34)	ATTTTTCGTTCGATGATA (SEQ ID NO: 707)
272	MSH3 (SEQ ID NO: 34)	ATTTTTTGTTTGATGATA (SEQ ID NO: 708)
273	MSH3 (SEQ ID NO: 34)	AGTTTAGTCGGGGTTATA (SEQ ID NO: 709)
274	MSH3 (SEQ ID NO: 34)	AGTTTAGTTGGGGTTATA (SEQ ID NO: 710)
275	MSH3 (SEQ ID NO: 34)	GGGTGAAGCGTTGAGGTT (SEQ ID NO: 711)
276	MSH3 (SEQ ID NO: 34)	GGGTGAAGTGTTGAGGTT (SEQ ID NO: 712)
277	MSH3 (SEQ ID NO: 34)	AGTATTTTCGTTTGAGGA (SEQ ID NO: 1015)
278	MSH3 (SEQ ID NO: 34)	AGTATTTTTGTTTGAGGA (SEQ ID NO: 1016)
279	MYC	TTAGAGTGTTCGGTTGTT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 35)	(SEQ ID NO: 713)
280	MYC (SEQ ID NO: 35)	TTAGAGTGTTTGGTTGTT (SEQ ID NO: 714)
281	MYC (SEQ ID NO: 35)	TTATAATGCGAGGGTTTG (SEQ ID NO: 1019)
282	MYC (SEQ ID NO: 35)	TTATAATGTGAGGGTTTG (SEQ ID NO: 1020)
283	MYC (SEQ ID NO: 35)	AGGATTTTCGAGTTGTGT (SEQ ID NO: 715)
284	MYC (SEQ ID NO: 35)	AGGATTTTTGAGTTGTGT (SEQ ID NO: 716)
285	MYC (SEQ ID NO: 35)	AATTTTAGCGAGAGGTAG (SEQ ID NO: 717)
286	MYC (SEQ ID NO: 35)	AATTTTAGTGAGAGGTAG (SEQ ID NO: 718)
287	N33 (SEQ ID NO: 36)	TTGGTTCGGGAAAGGTAA (SEQ ID NO: 977)
288	N33 (SEQ ID NO: 36)	TTGGTTTGGGAAAGGTAA (SEQ ID NO: 978)
289	N33 (SEQ ID NO: 36)	TGTTATTTCGGAGGGTTT (SEQ ID NO: 909)
290	N33 (SEQ ID NO: 36)	TGTTATTTTGGAGGGTTT (SEQ ID NO: 910)
291	N33 (SEQ ID NO: 36)	GTTTAGTTAGCGGGTTTT (SEQ ID NO: 943)
292	N33 (SEQ ID NO: 36)	GTTTAGTTAGTGGGTTTT (SEQ ID NO: 944)
293	N33 (SEQ ID NO: 36)	ATTTAGTTCGGGGGAGGA (SEQ ID NO: 993)
294	N33 (SEQ ID NO: 36)	ATTTAGTTTGGGGGAGGA (SEQ ID NO: 994)
295	PAX6 (SEQ ID NO: 37)	TATTGTTTCGGTTGTTAG (SEQ ID NO: 719)
296	PAX6 (SEQ ID NO: 37)	TATTGTTTTGGTTGTTAG (SEQ ID NO: 720)
297	PAX6 (SEQ ID NO: 37)	GTTAGTAGCGAGTTTAGG (SEQ ID NO: 721)
298	PAX6 (SEQ ID NO: 37)	GTTAGTAGTGAGTTTAGG (SEQ ID NO: 722)
299	PAX6 (SEQ ID NO: 37)	AGAGTTTAGCGTATTTTT (SEQ ID NO: 723)
300	PAX6 (SEQ ID NO: 37)	AGAGTTTAGTGTATTTTT (SEQ ID NO: 724)
301	PGR (SEQ ID NO: 38)	GAATTTAGCGAGGGATTG (SEQ ID NO: 725)
302	PGR (SEQ ID NO: 38)	GAATTTAGTGAGGGATTG (SEQ ID NO: 726)
303	PGR (SEQ ID NO: 38)	AGTATGTACGAGTTTGAT (SEQ ID NO: 727)
304	PGR	AGTATGTATGAGTTTGAT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 38)	(SEQ ID NO: 728)
305	PGR (SEQ ID NO: 38)	TTAAGTGTCGGATTTGTG (SEQ ID NO: 1011)
306	PGR (SEQ ID NO: 38)	TTAAGTGTTGGATTTGTG (SEQ ID NO: 1012)
307	PGR (SEQ ID NO: 38)	GGGATAAACGATAGTTAT (SEQ ID NO: 729)
308	PGR (SEQ ID NO: 38)	GGGATAAATGATAGTTAT (SEQ ID NO: 730)
309	PTEN (SEQ ID NO: 39)	AGAGTTTGCGGTTTGGGG (SEQ ID NO: 731)
310	PTEN (SEQ ID NO: 39)	AGAGTTTGTGGTTTGGGGT (SEQ ID NO: 732)
311	PTEN (SEQ ID NO: 39)	ATTTTGCGTTCGTATTTA (SEQ ID NO: 987)
312	PTEN (SEQ ID NO: 39)	ATTTTGTGTTTGTATTTA (SEQ ID NO: 988)
313	PTEN (SEQ ID NO: 39)	AGAGTTATCGTTTTGTTT (SEQ ID NO: 957)
314	PTEN (SEQ ID NO: 39)	AGAGTTATTGTTTTGTTT (SEQ ID NO: 958)
315	PTEN (SEQ ID NO: 39)	TGATGTGGCGGGATTTTT (SEQ ID NO: 947)
316	PTEN (SEQ ID NO: 39)	TGATGTGGTGGGATTTTT (SEQ ID NO: 948)
317	RARB (SEQ ID NO: 40)	TAGTAGTTCGGGTAGGGT (SEQ ID NO: 991)
318	RARB (SEQ ID NO: 40)	TAGTAGTTTGGGTAGGGT (SEQ ID NO: 992)
319	RARB (SEQ ID NO: 40)	GGGTTTATCGAAAGTTTA (SEQ ID NO: 733)
320	RARB (SEQ ID NO: 40)	GGGTTTATTGAAAGTTTA (SEQ ID NO: 734)
321	RARB (SEQ ID NO: 40)	AGTTTATTCGTATATATT (SEQ ID NO: 735)
322	RARB (SEQ ID NO: 40)	AGTTTATTTGTATATATT (SEQ ID NO: 736)
323	RARB (SEQ ID NO: 40)	TTTTTATGCGAGTTGTTT (SEQ ID NO: 737)
324	RARB (SEQ ID NO: 40)	TTTTTATGTGAGTTGTTT (SEQ ID NO: 738)
325	SFN (SEQ ID NO: 41)	ATAGAGTTCGGTATTGGT (SEQ ID NO: 739)
326	SFN (SEQ ID NO: 41)	ATAGAGTTTGGTATTGGT (SEQ ID NO: 740)
327	SFN (SEQ ID NO: 41)	GTAGGTCGAACGTTATGA (SEQ ID NO: 741)
328	SFN (SEQ ID NO: 41)	GTAGGTTGAATGTTATGA (SEQ ID NO: 742)
329	SFN	AAAAGTAACGAGGAGGGT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 41)	(SEQ ID NO: 743)
330	SFN (SEQ ID NO: 41)	AAAAGTAATGAGGAGGGT (SEQ ID NO: 744)
331	S100A2 (SEQ ID NO: 42)	TTTAATTGCGGTTGTGTG (SEQ ID NO: 745)
332	S100A2 (SEQ ID NO: 42)	TTTAATTGTGGTTGTGTG (SEQ ID NO: 746)
333	S100A2 (SEQ ID NO: 42)	TATATAGGCGTATGTATG (SEQ ID NO: 747)
334	S100A2 (SEQ ID NO: 42)	TATATAGGTGTATGTATG (SEQ ID NO: 748)
335	S100A2 (SEQ ID NO: 42)	TATGTATACGAGTATTGG (SEQ ID NO: 999)
336	S100A2 (SEQ ID NO: 42)	TATGTATATGAGTATTGG (SEQ ID NO: 1000)
337	S100A2 (SEQ ID NO: 42)	AGTTTTAGCGTGTGTTTA (SEQ ID NO: 749)
338	S100A2 (SEQ ID NO: 42)	AGTTTTAGTGTGTGTTTA (SEQ ID NO: 750)
339	TGFBR2 (SEQ ID NO: 43)	ATTTGGAGCGAGGAATTT (SEQ ID NO: 751)
340	TGFBR2 (SEQ ID NO: 43)	ATTTGGAGTGAGGAATTT (SEQ ID NO: 752)
341	TGFBR2 (SEQ ID NO: 43)	TTGAAAGTCGGTTAAAGT (SEQ ID NO: 753)
342	TGFBR2 (SEQ ID NO: 43)	TTGAAAGTTGGTTAAAGT (SEQ ID NO: 754)
343	TGFBR2 (SEQ ID NO: 43)	AAAGTTTTCGGAGGGGTT (SEQ ID NO: 907)
344	TGFBR2 (SEQ ID NO: 43)	AAAGTTTTTGGAGGGGTT (SEQ ID NO: 908)
345	TGFBR2 (SEQ ID NO: 43)	GGTAGTTACGAGAGAGTT (SEQ ID NO: 755)
346	TGFBR2 (SEQ ID NO: 43)	GGTAGTTATGAGAGAGTT (SEQ ID NO: 756)
347	TIMP3 (SEQ ID NO: 44)	AGGTTTTTCGTTGGAGAA (SEQ ID NO: 757)
348	TIMP3 (SEQ ID NO: 44)	AGGTTTTTTGTTGGAGAA (SEQ ID NO: 758)
349	TIMP3 (SEQ ID NO: 44)	GAAAATATCGGTATTTTG (SEQ ID NO: 759)
350	TIMP3 (SEQ ID NO: 44)	GAAAATATTGGTATTTTG (SEQ ID NO: 760)
351	TIMP3 (SEQ ID NO: 44)	GGGATAAGCGAATTTTTT (SEQ ID NO: 761)
352	TIMP3 (SEQ ID NO: 44)	GGGATAAGTGAATTTTTT (SEQ ID NO: 762)
353	TIMP3 (SEQ ID NO: 44)	TTTTATTACGTATGTTTT (SEQ ID NO: 763)
354	TIMP3	TTTTATTATGTATGTTTT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 44)	(SEQ ID NO: 764)
355	TP53 (SEQ ID NO: 45)	AAGTTGAACGTTTAGGTA (SEQ ID NO: 765)
356	TP53 (SEQ ID NO: 45)	AAGTTGAATGTTTAGGTA (SEQ ID NO: 766)
357	TP53 (SEQ ID NO: 45)	TTTTGAGTCGGTTTAAAG (SEQ ID NO: 767)
358	TP53 (SEQ ID NO: 45)	TTTTGAGTTGGTTTAAAG (SEQ ID NO: 768)
359	TP53 (SEQ ID NO: 45)	TATTTATTCGGTGTTGGG (SEQ ID NO: 769)
360	TP53 (SEQ ID NO: 45)	TATTTATTTGGTGTTGGG (SEQ ID NO: 770)
361	TP53 (SEQ ID NO: 45)	TTGGATTTCGAAATATTG (SEQ ID NO: 771)
362	TP53 (SEQ ID NO: 45)	TTGGATTTTGAAATATTG (SEQ ID NO: 772)
363	TP73 (SEQ ID NO: 46)	TGATTTAGCGTAGGTTTG (SEQ ID NO: 773)
364	TP73 (SEQ ID NO: 46)	TGATTTAGTGTAGGTTTG (SEQ ID NO: 774)
365	TP73 (SEQ ID NO: 46)	TTAGAGTTCGAGTTTATA (SEQ ID NO: 775)
366	TP73 (SEQ ID NO: 46)	TTAGAGTTTGAGTTTATA (SEQ ID NO: 776)
367	TP73 (SEQ ID NO: 46)	AAGTTACGGGTTTTATTG (SEQ ID NO: 915)
368	TP73 (SEQ ID NO: 46)	AAGTTATGGGTTTTATTG (SEQ ID NO: 916)
369	TP73 (SEQ ID NO: 46)	GGAAGTTTCGATGGTTTA (SEQ ID NO: 777)
370	TP73 (SEQ ID NO: 46)	GGAAGTTTTGATGGTTTA (SEQ ID NO: 778)
371	VHL (SEQ ID NO: 47)	TTTATAAGCGTGATGATT (SEQ ID NO: 779)
372	VHL (SEQ ID NO: 47)	TTTATAAGTGTGATGATT (SEQ ID NO: 780)
373	VHL (SEQ ID NO: 47)	GGTGTTTTCGTGTGAGAT (SEQ ID NO: 781)
374	VHL (SEQ ID NO: 47)	GGTGTTTTTGTGTGAGAT (SEQ ID NO: 782)
375	VHL (SEQ ID NO: 47)	TGTGAGATGCGTTATTTT (SEQ ID NO: 783)
376	VHL (SEQ ID NO: 47)	TGTGAGATGTGTTATTTT (SEQ ID NO: 784)
377	VHL (SEQ ID NO: 47)	TATATTGCGCGTTTGATA (SEQ ID NO: 785)
378	VHL (SEQ ID NO: 47)	TATATTGTGTGTTTGATA (SEQ ID NO: 786)
379	CDKN1C	ATGAAGAACGGTTAAGGG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 48)	(SEQ ID NO: 787)
380	CDKN1C (SEQ ID NO: 48)	ATGAAGAATGGTTAAGGG (SEQ ID NO: 788)
381	CDKN1C (SEQ ID NO: 48)	TTTTATTTCGAGTTAGGT (SEQ ID NO: 789)
382	CDKN1C (SEQ ID NO: 48)	TTTTATTTTGAGTTAGGT (SEQ ID NO: 790)
383	CDKN1C (SEQ ID NO: 48)	TTAAGTTACGGTTATTAG (SEQ ID NO: 791)
384	CDKN1C (SEQ ID NO: 48)	TTAAGTTATGGTTATTAG (SEQ ID NO: 792)
385	CDKN1C (SEQ ID NO: 48)	TTAGTGTTCGTTTGGAAT (SEQ ID NO: 793)
386	CDKN1C (SEQ ID NO: 48)	TTAGTGTTTGTTTGGAAT (SEQ ID NO: 794)
387	CAV1 (SEQ ID NO: 49)	TTGGTATCGTTGAAGAAT (SEQ ID NO: 795)
388	CAV1 (SEQ ID NO: 49)	TTGGTATTGTTGAAGAAT (SEQ ID NO: 796)
389	CAV1 (SEQ ID NO: 49)	TAGATTCGGAGGTAGGTA (SEQ ID NO: 911)
390	CAV1 (SEQ ID NO: 49)	TAGATTTGGAGGTAGGTA (SEQ ID NO: 912)
391	CAV1 (SEQ ID NO: 49)	TGGGGGTTCGAAAAAGTG (SEQ ID NO: 797)
392	CAV1 (SEQ ID NO: 49)	TGGGGGTTTGAAAAAGTG (SEQ ID NO: 798)
393	CAV1 (SEQ ID NO: 49)	GAAGTGTTCGTTTTTGTT (SEQ ID NO: 799)
394	CAV1 (SEQ ID NO: 49)	GAAGTGTTTGTTTTTGTT (SEQ ID NO: 800)
395	CDH13 (SEQ ID NO: 50)	GAAGTGGTCGTTAGTTTT (SEQ ID NO: 801)
396	CDH13 (SEQ ID NO: 50)	GAAGTGGTTGTTAGTTTTT (SEQ ID NO: 802)
397	CDH13 (SEQ ID NO: 50)	TTGTTTAGCGTGATTTGT (SEQ ID NO: 803)
398	CDH13 (SEQ ID NO: 50)	TTGTTTAGTGTGATTTGT (SEQ ID NO: 804)
399	CDH13 (SEQ ID NO: 50)	AAGGAATTCGTTTTGTAA (SEQ ID NO: 903)
400	CDH13 (SEQ ID NO: 50)	AAGGAATTTGTTTTGTAA (SEQ ID NO: 904)
401	CDH13 (SEQ ID NO: 50)	AATGTTTTCGTGATGTTG (SEQ ID NO: 895)
402	CDH13 (SEQ ID NO: 50)	AATGTTTTTGTGATGTTG (SEQ ID NO: 896)
403	DRG1 (SEQ ID NO: 51)	GAGTAGGACGGTGTTAAG (SEQ ID NO: 805)
404	DRG1	GAGTAGGATGGTGTTAAG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 51)	(SEQ ID NO: 806)
405	DRG1 (SEQ ID NO: 51)	AAATTTAACGTTGGGTAG (SEQ ID NO: 807)
406	DRG1 (SEQ ID NO: 51)	AAATTTAATGTTGGGTAG (SEQ ID NO: 808)
407	DRG1 (SEQ ID NO: 51)	GATAATGACGGTGTTAGT (SEQ ID NO: 809)
408	DRG1 (SEQ ID NO: 51)	GATAATGATGGTGTTAGT (SEQ ID NO: 810)
409	DRG1 (SEQ ID NO: 51)	TGGTTGTACGTTAGGAGT (SEQ ID NO: 811)
410	DRG1 (SEQ ID NO: 51)	TGGTTGTATGTTAGGAGT (SEQ ID NO: 812)
411	PTGS2 (SEQ ID NO: 52)	TTTATTTTCGTGGGTAAA (SEQ ID NO: 913)
412	PTGS2 (SEQ ID NO: 52)	TTTATTTTTGTGGGTAAA (SEQ ID NO: 914)
413	PTGS2 (SEQ ID NO: 52)	AGTTATTTCGTTATATGG (SEQ ID NO: 1007)
414	PTGS2 (SEQ ID NO: 52)	AGTTATTTTGTTATATGG (SEQ ID NO: 1008)
415	PTGS2 (SEQ ID NO: 52)	ATTTAAGGCGATTAGTTT (SEQ ID NO: 813)
416	PTGS2 (SEQ ID NO: 52)	ATTTAAGGTGATTAGTTT (SEQ ID NO: 814)
417	PTGS2 (SEQ ID NO: 52)	ATATTTGGCGGAAATTTG (SEQ ID NO: 1023)
418	PTGS2 (SEQ ID NO: 52)	ATATTTGGTGGAAATTTG (SEQ ID NO: 1024)
419	THBS1 (SEQ ID NO: 53)	GGAGAGTTAGCGAGGGTT (SEQ ID NO: 815)
420	THBS1 (SEQ ID NO: 53)	GGAGAGTTAGTGAGGGTT (SEQ ID NO: 816)
421	THBS1 (SEQ ID NO: 53)	TATTTTAACGAATGGTTT (SEQ ID NO: 817)
422	THBS1 (SEQ ID NO: 53)	TATTTTAATGAATGGTTT (SEQ ID NO: 818)
423	THBS1 (SEQ ID NO: 53)	TTATAAAACGGGTTTAGT (SEQ ID NO: 819)
424	THBS1 (SEQ ID NO: 53)	TTATAAAATGGGTTTAGT (SEQ ID NO: 820)
425	THBS1 (SEQ ID NO: 53)	AGGTATTTCGGGAGATTA (SEQ ID NO: 821)
426	THBS1 (SEQ ID NO: 53)	AGGTATTTTGGGAGATTA (SEQ ID NO: 822)
427	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATTTGTTTCGATTAATTT (SEQ ID NO: 979)
428	TPEF (=TMEFF2; =HPP1)	ATTTGTTTTGATTAATTT (SEQ ID NO: 980)

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 54)	
429	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTACGGGTTGGAG (SEQ ID NO: 917)
430	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTATGGGTTGGAG (SEQ ID NO: 918)
431	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGCGAACGTTTGGG (SEQ ID NO: 899)
432	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGTGAATGTTTGGG (SEQ ID NO: 900)
433	DNMT1 (SEQ ID NO: 55)	AGTGGGTTCGTTTAAGTT (SEQ ID NO: 823)
434	DNMT1 (SEQ ID NO: 55)	AGTGGGTTTGTTTAAGTT (SEQ ID NO: 824)
435	DNMT1 (SEQ ID NO: 55)	TTTTTTACGCGGAGTAGT (SEQ ID NO: 825)
436	DNMT1 (SEQ ID NO: 55)	TTTTTTATGTGGAGTAGT (SEQ ID NO: 826)
437	DNMT1 (SEQ ID NO: 55)	GAGAGAGGCGATATTTTG (SEQ ID NO: 827)
438	DNMT1 (SEQ ID NO: 55)	GAGAGAGGTGATATTTTG (SEQ ID NO: 828)
439	DNMT1 (SEQ ID NO: 55)	GTATTAAACGGAGAGAGG (SEQ ID NO: 829)
440	DNMT1 (SEQ ID NO: 55)	GTATTAAATGGAGAGAGG (SEQ ID NO: 830)
441	CEA (SEQ ID NO: 56)	AAGTGTTCGCGGTTGTTT (SEQ ID NO: 1003)
442	CEA (SEQ ID NO: 56)	AAGTGTTTGTGGTTGTTT (SEQ ID NO: 1004)
443	CEA (SEQ ID NO: 56)	TTTTGAGTCGTAGTTTAG (SEQ ID NO: 831)
444	CEA (SEQ ID NO: 56)	TTTTGAGTTGTAGTTTAG (SEQ ID NO: 832)
445	CEA (SEQ ID NO: 56)	AATAGATACGGAGAGGGA (SEQ ID NO: 833)
446	CEA (SEQ ID NO: 56)	AATAGATATGGAGAGGGA (SEQ ID NO: 834)
447	MB (SEQ ID NO: 57)	AGAAGGTGCGTGAGAGGT (SEQ ID NO: 835)
448	MB (SEQ ID NO: 57)	AGAAGGTGTGTGAGAGGT (SEQ ID NO: 836)
449	MB (SEQ ID NO: 57)	GGGTTAGTCGGGGTATTT (SEQ ID NO: 837)
450	MB (SEQ ID NO: 57)	GGGTTAGTTGGGGTATTT (SEQ ID NO: 838)
451	MB	GGGGATAGCGAGTTATTG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 57)	(SEQ ID NO: 839)
452	MB (SEQ ID NO: 57)	GGGGATAGTGAGTTATTG (SEQ ID NO: 840)
453	MB (SEQ ID NO: 57)	TTAGATTGCGTTATGGGG (SEQ ID NO: 841)
454	MB (SEQ ID NO: 57)	TTAGATTGTGTTATGGGG (SEQ ID NO: 842)
455	PCNA (SEQ ID NO: 58)	TAAAGAGGCGGGGAGATT (SEQ ID NO: 1013)
456	PCNA (SEQ ID NO: 58)	TAAAGAGGTGGGGAGATT (SEQ ID NO: 1014)
457	PCNA (SEQ ID NO: 58)	TATGGATACGATTGGTTT (SEQ ID NO: 843)
458	PCNA (SEQ ID NO: 58)	TATGGATATGATTGGTTT (SEQ ID NO: 844)
459	PCNA (SEQ ID NO: 58)	GTATTAAACGGTTGTAGG (SEQ ID NO: 845)
460	PCNA (SEQ ID NO: 58)	GTATTAAATGGTTGTAGG (SEQ ID NO: 846)
461	PCNA (SEQ ID NO: 58)	TTTGAAGTCGAAATTAGT (SEQ ID NO: 847)
462	PCNA (SEQ ID NO: 58)	TTTGAAGTTGAAATTAGT (SEQ ID NO: 848)
463	CDC2 (SEQ ID NO: 59)	TGGAATTTCGATGTAAAT (SEQ ID NO: 849)
464	CDC2 (SEQ ID NO: 59)	TGGAATTTTGATGTAAAT (SEQ ID NO: 850)
465	CDC2 (SEQ ID NO: 59)	TAGTAGGACGATATTTTT (SEQ ID NO: 851)
466	CDC2 (SEQ ID NO: 59)	TAGTAGGATGATATTTTT (SEQ ID NO: 852)
467	CDC2 (SEQ ID NO: 59)	TAGTTATTCGGGAAGGTT (SEQ ID NO: 853)
468	CDC2 (SEQ ID NO: 59)	TAGTTATTTGGGAAGGTT (SEQ ID NO: 854)
469	CDC2 (SEQ ID NO: 59)	AAATTGTTCGTATTTGGT (SEQ ID NO: 855)
470	CDC2 (SEQ ID NO: 59)	AAATTGTTTGTATTTGGT (SEQ ID NO: 856)
471	ESR1 (SEQ ID NO: 60)	AGATATATCGGAGTTTGG (SEQ ID NO: 857)
472	ESR1 (SEQ ID NO: 60)	AGATATATTGGAGTTTGG (SEQ ID NO: 858)
473	ESR1 (SEQ ID NO: 60)	GTTTGGTACGGGGTATAT (SEQ ID NO: 859)
474	ESR1 (SEQ ID NO: 60)	GTTTGGTATGGGGTATAT (SEQ ID NO: 860)
475	ESR1 (SEQ ID NO: 60)	TTTTAAATCGAGTTGTGT (SEQ ID NO: 861)
476	ESR1	TTTTAAATTGAGTTGTGT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 60)	(SEQ ID NO: 862)
477	ESR1 (SEQ ID NO: 60)	TATGAGTTCGGGAGATTA (SEQ ID NO: 863)
478	ESR1 (SEQ ID NO: 60)	TATGAGTTTGGGAGATTA (SEQ ID NO: 864)
479	ESR1 (SEQ ID NO: 60)	TGGAGGTTCGGGAGTTTA (SEQ ID NO: 969)
480	ESR1 (SEQ ID NO: 60)	TGGAGGTTTGGGAGTTTA (SEQ ID NO: 970)
481	CASP8 (SEQ ID NO: 61)	GAATGAGTCGAGGAAGGT (SEQ ID NO: 865)
482	CASP8 (SEQ ID NO: 61)	GAATGAGTTGAGGAAGGT (SEQ ID NO: 866)
483	CASP8 (SEQ ID NO: 61)	TATTGAGACGTTAAGTAA (SEQ ID NO: 867)
484	CASP8 (SEQ ID NO: 61)	TATTGAGATGTTAAGTAA (SEQ ID NO: 868)
485	CASP8 (SEQ ID NO: 61)	TAAGGTTACGTAGTTAGT (SEQ ID NO: 869)
486	CASP8 (SEQ ID NO: 61)	TAAGGTTATGTAGTTAGT (SEQ ID NO: 870)
487	CASP8 (SEQ ID NO: 61)	GTTAATAGCGGGGATTTT (SEQ ID NO: 871)
488	CASP8 (SEQ ID NO: 61)	GTTAATAGTGGGGATTTT (SEQ ID NO: 872)
489	RASSF1 (SEQ ID NO: 62)	GTAGTTTTCGAGAATGTT (SEQ ID NO: 873)
490	RASSF1 (SEQ ID NO: 62)	GTAGTTTTTGAGAATGTT (SEQ ID NO: 874)
491	RASSF1 (SEQ ID NO: 62)	TAATTAGAACGTTTTTTG (SEQ ID NO: 875)
492	RASSF1 (SEQ ID NO: 62)	TAATTAGAATGTTTTTTG (SEQ ID NO: 876)
493	RASSF1 (SEQ ID NO: 62)	TAGTTTTCGCGTAGAATT (SEQ ID NO: 877)
494	RASSF1 (SEQ ID NO: 62)	TAGTTTTTGTGTAGAATT (SEQ ID NO: 878)
495	RASSF1 (SEQ ID NO: 62)	TTTGTAGCGGGTGGAGTA (SEQ ID NO: 995)
496	RASSF1 (SEQ ID NO: 62)	TTTGTAGTGGGTGGAGTA (SEQ ID NO: 996)
497	MSH4 (SEQ ID NO: 63)	TTGTTTCGGCGGTTTTTT (SEQ ID NO: 879)
498	MSH4 (SEQ ID NO: 63)	TTGTTTTGGTGGTTTTTT (SEQ ID NO: 880)
499	MSH4 (SEQ ID NO: 63)	TTTTGGTACGTTAGGAGT (SEQ ID NO: 881)
500	MSH4 (SEQ ID NO: 63)	TTTTGGTATGTTAGGAGT (SEQ ID NO: 882)
501	MSH4	TAAATTTTCGGTTAGTTT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 63)	(SEQ ID NO: 883)
502	MSH4 (SEQ ID NO: 63)	TAAATTTTTGGTTAGTTT (SEQ ID NO: 884)
503	MSH4 (SEQ ID NO: 63)	TTAGAGGTCGGTAGTTTA (SEQ ID NO: 885)
504	MSH4 (SEQ ID NO: 63)	TTAGAGGTTGGTAGTTTA (SEQ ID NO: 886)
505	MSH5 (SEQ ID NO: 64)	ATGTTTATCGTTTTGAGT (SEQ ID NO: 887)
506	MSH5 (SEQ ID NO: 64)	ATGTTTATTGTTTTGAGT (SEQ ID NO: 888)
507	MSH5 (SEQ ID NO: 64)	ATAGTTGTCGAATGTATG (SEQ ID NO: 889)
508	MSH5 (SEQ ID NO: 64)	ATAGTTGTTGAATGTATG (SEQ ID NO: 890)
509	MSH5 (SEQ ID NO: 64)	TAGAAGTGCGAAGGGGTA (SEQ ID NO: 891)
510	MSH5 (SEQ ID NO: 64)	TAGAAGTGTGAAGGGGTA (SEQ ID NO: 892)
511	MSH5 (SEQ ID NO: 64)	ATGTAATTCGAATGTTTT (SEQ ID NO: 893)
512	MSH5 (SEQ ID NO: 64)	ATGTAATTTGAATGTTTT (SEQ ID NO: 894)

Table 3: Oligonucleotides used in differentiation between colon adenomas or carcinoma tissue and healthy colon tissue.

No:	*Gene*	*Oligo:*
1	CDH13 (SEQ ID NO: 50)	AATGTTTTCGTGATGTTG (SEQ ID NO: 895)
2	CDH13 (SEQ ID NO: 50)	AATGTTTTTGTGATGTTG (SEQ ID NO: 896)
3	CD44 (SEQ ID NO: 20)	TTGTTTAGCGGATTTTAG (SEQ ID NO: 897)
4	CD44 (SEQ ID NO: 20)	TTGTTTAGTGGATTTTAG (SEQ ID NO: 898)
5	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGCGAACGTTTGGG (SEQ ID NO: 899)
6	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGTGAATGTTTGGG (SEQ ID NO: 900)
7	CSPG2 (SEQ ID NO: 21)	GGGTAACGTCGAATTTAG (SEQ ID NO: 901)
8	CSPG2 (SEQ ID NO: 21)	GGGTAATGTTGAATTTAG (SEQ ID NO: 902)
9	CDH13 (SEQ ID NO: 50)	AAGGAATTCGTTTTGTAA (SEQ ID NO: 903)
10	CDH13	AAGGAATTTGTTTTGTAA

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 50)	(SEQ ID NO: 904)
11	GSTP1 (SEQ ID NO: 25)	GGAGTTCGCGGGATTTTT (SEQ ID NO: 905)
12	GSTP1 (SEQ ID NO: 25)	GGAGTTTGTGGGATTTTT (SEQ ID NO: 906)
13	TGFBR2 (SEQ ID NO: 43)	AAAGTTTTCGGAGGGGTT (SEQ ID NO: 907)
14	TGFBR2 (SEQ ID NO: 43)	AAAGTTTTTGGAGGGGTT (SEQ ID NO: 908)
15	N33 (SEQ ID NO: 36)	TGTTATTTCGGAGGGTTT (SEQ ID NO: 909)
16	N33 (SEQ ID NO: 36)	TGTTATTTTGGAGGGTTT (SEQ ID NO: 910)
17	CAV1 (SEQ ID NO: 49)	TAGATTCGGAGGTAGGTA (SEQ ID NO: 911)
18	CAV1 (SEQ ID NO: 49)	TAGATTTGGAGGTAGGTA (SEQ ID NO: 912)
19	PTGS2 (SEQ ID NO: 52)	TTTATTTTCGTGGGTAAA (SEQ ID NO: 913)
20	PTGS2 (SEQ ID NO: 52)	TTTATTTTTGTGGGTAAA (SEQ ID NO: 914)
21	TP73 (SEQ ID NO: 46)	AAGTTACGGGTTTTATTG (SEQ ID NO: 915)
22	TP73 (SEQ ID NO: 46)	AAGTTATGGGTTTTATTG (SEQ ID NO: 916)
23	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTACGGGTTGGAG (SEQ ID NO: 917)
24	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTATGGGTTGGAG (SEQ ID NO: 918)
25	CD44 (SEQ ID NO: 20)	GTGGGGTTCGGAGGTATA (SEQ ID NO: 919)
26	CD44 (SEQ ID NO: 20)	GTGGGGTTTGGAGGTATA (SEQ ID NO: 920)
27	EYA4 (SEQ ID NO: 24)	AAGTAAGTCGTTGTTGTT (SEQ ID NO: 921)
28	EYA4 (SEQ ID NO: 24)	AAGTAAGTTGTTGTTGTT (SEQ ID NO: 922)
29	EYA4 (SEQ ID NO: 24)	AGTGTATGCGTAGAAGGT (SEQ ID NO: 923)
30	EYA4 (SEQ ID NO: 24)	AGTGTATGTGTAGAAGGT (SEQ ID NO: 924)
31	GTBP/MSH6 (SEQ ID NO: 26)	TTTGTTGGCGGGAAATTT (SEQ ID NO: 925)
32	GTBP/MSH6 (SEQ ID NO: 26)	TTTGTTGGTGGGAAATTT (SEQ ID NO: 926)
33	EGR4 (SEQ ID NO: 4)	GGAGTTTTCGGTATATAT (SEQ ID NO: 927)
34	EGR4	GGAGTTTTTGGTATATAT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 4)	(SEQ ID NO: 928)
35	CDH1 (SEQ ID NO: 15)	TAGTGGCGTCGGAATTGT (SEQ ID NO: 929)
36	CDH1 (SEQ ID NO: 15)	TAGTGGTGTTGGAATTGT (SEQ ID NO: 930)
37	EGFR (SEQ ID NO: 23)	ATTTGGTTCGATTTGGAT (SEQ ID NO: 931)
38	EGFR (SEQ ID NO: 23)	ATTTGGTTTGATTTGGAT (SEQ ID NO: 932)
39	LKB1 (SEQ ID NO: 30)	AGGGAGGTCGTTGGTATT (SEQ ID NO: 933)
40	LKB1 (SEQ ID NO: 30)	AGGGAGGTTGTTGGTATT (SEQ ID NO: 934)
41	DAPK1 (SEQ ID NO: 22)	TTGTTTTTCGGAAATTTG (SEQ ID NO: 935)
42	DAPK1 (SEQ ID NO: 22)	TTGTTTTTTGGAAATTTG (SEQ ID NO: 936)
43	IGF2 (SEQ ID NO: 29)	GATTAGGGCGGGAAATAT (SEQ ID NO: 937)
44	IGF2 (SEQ ID NO: 29)	GATTAGGGTGGGAAATAT (SEQ ID NO: 938)
45	HLA-F (SEQ ID NO: 10)	TATTTGGGCGGGTGAGTG (SEQ ID NO: 939)
46	HLA-F (SEQ ID NO: 10)	TATTTGGGTGGGTGAGTG (SEQ ID NO: 940)
47	IGF2 (SEQ ID NO: 29)	TTGTATGGTCGAGTTTAT (SEQ ID NO: 941)
48	IGF2 (SEQ ID NO: 29)	TTGTATGGTTGAGTTTAT (SEQ ID NO: 942)
49	N33 (SEQ ID NO: 36)	GTTTAGTTAGCGGGTTTT (SEQ ID NO: 943)
50	N33 (SEQ ID NO: 36)	GTTTAGTTAGTGGGTTTT (SEQ ID NO: 944)
51	CSPG2 (SEQ ID NO: 21)	AAAAATTCGCGAGTTTAG (SEQ ID NO: 945)
52	CSPG2 (SEQ ID NO: 21)	AAAAATTTGTGAGTTTAG (SEQ ID NO: 946)
53	PTEN (SEQ ID NO: 39)	TGATGTGGCGGGATTTTT (SEQ ID NO: 947)
54	PTEN (SEQ ID NO: 39)	TGATGTGGTGGGATTTTT (SEQ ID NO: 948)
55	MLH1 (SEQ ID NO: 32)	TTAGGTAGCGGGTAGTAG (SEQ ID NO: 949)
56	MLH1 (SEQ ID NO: 32)	TTAGGTAGTGGGTAGTAG (SEQ ID NO: 950)
57	GTBP/MSH6 (SEQ ID NO: 26)	GAGGAATTCGGGTTTTAG (SEQ ID NO: 951)
58	GTBP/MSH6 (SEQ ID NO: 26)	GAGGAATTTGGGTTTTAG (SEQ ID NO: 952)
59	CALCA	ATTAGGTTCGTGTTTTAG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 14)	(SEQ ID NO: 953)
60	CALCA (SEQ ID NO: 14)	ATTAGGTTTGTGTTTTAG (SEQ ID NO: 954)
61	DAPK1 (SEQ ID NO: 22)	GAAGGGAGCGTATTTTAT (SEQ ID NO: 955)
62	DAPK1 (SEQ ID NO: 22)	GAAGGGAGTGTATTTTAT (SEQ ID NO: 956)
63	PTEN (SEQ ID NO: 39)	AGAGTTATCGTTTTGTTT (SEQ ID NO: 957)
64	PTEN (SEQ ID NO: 39)	AGAGTTATTGTTTTGTTT (SEQ ID NO: 958)
65	WT1 (SEQ ID NO: 9)	TGTTATATCGGTTAGTTG (SEQ ID NO: 959)
66	WT1 (SEQ ID NO: 9)	TGTTATATTGGTTAGTTG (SEQ ID NO: 960)
67	EGFR (SEQ ID NO: 23)	TTTGTATTCGGAGTTGGG (SEQ ID NO: 961)
68	EGFR (SEQ ID NO: 23)	TTTGTATTTGGAGTTGGG (SEQ ID NO: 962)
69	CSPG2 (SEQ ID NO: 21)	AAGATTTTCGGTTAGTTT (SEQ ID NO: 963)
70	CSPG2 (SEQ ID NO: 21)	AAGATTTTTGGTTAGTTT (SEQ ID NO: 964)
71	LKB1 (SEQ ID NO: 30)	TTTAGGTTCGTAAGTTTA (SEQ ID NO: 965)
72	LKB1 (SEQ ID NO: 30)	TTTAGGTTTGTAAGTTTA (SEQ ID NO: 966)
73	WT1 (SEQ ID NO: 9)	TATATTGGCGAAGGTTAA (SEQ ID NO: 967)
74	WT1 (SEQ ID NO: 9)	TATATTGGTGAAGGTTAA (SEQ ID NO: 968)
75	ESR1 (SEQ ID NO: 60)	TGGAGGTTCGGGAGTTTA (SEQ ID NO: 969)
76	ESR1 (SEQ ID NO: 60)	TGGAGGTTTGGGAGTTTA (SEQ ID NO: 970)
77	APC (SEQ ID NO: 12)	TTTAATCGTATAGTTTGT (SEQ ID NO: 971)
78	APC (SEQ ID NO: 12)	TTTAATTGTATAGTTTGT (SEQ ID NO: 972)
79	IGF2 (SEQ ID NO: 29)	AGTTTGAACGATGTAAGA (SEQ ID NO: 973)
80	IGF2 (SEQ ID NO: 29)	AGTTTGAATGATGTAAGA (SEQ ID NO: 974)
81	MYOD1 (SEQ ID NO: 8)	AATTAGGTCGGATAGGAG (SEQ ID NO: 975)
82	MYOD1 (SEQ ID NO: 8)	AATTAGGTTGGATAGGAG (SEQ ID NO: 976)
83	N33 (SEQ ID NO: 36)	TTGGTTCGGGAAAGGTAA (SEQ ID NO: 977)
84	N33	TTGGTTTGGGAAAGGTAA

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 36)	(SEQ ID NO: 978)
85	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATTTGTTTCGATTAATTT (SEQ ID NO: 979)
86	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATTTGTTTTGATTAATTT (SEQ ID NO: 980)
87	CDKN2a (SEQ ID NO: 18)	AATAGTTACGGTCGGAGG (SEQ ID NO: 981)
88	CDKN2a (SEQ ID NO: 18)	AATAGTTATGGTTGGAGG (SEQ ID NO: 982)
89	CDH1 (SEQ ID NO: 15)	AGGGTTATCGCGTTTATG (SEQ ID NO: 983)
90	CDH1 (SEQ ID NO: 15)	AGGGTTATTGTGTTTATG (SEQ ID NO: 984)
91	APC (SEQ ID NO: 12)	TATTTTGGCGGGTTGTAT (SEQ ID NO: 985)
92	APC (SEQ ID NO: 12)	TATTTTGGTGGGTTGTAT (SEQ ID NO: 986)

Table 4: Oligonucleotides used in differentiation between colon carcinoma tissue and healthy colon tissue.

No:	*Gene*	*Oligo:*
1	CDH13 (SEQ ID NO: 50)	AATGTTTTCGTGATGTTG (SEQ ID NO: 895)
2	CDH13 (SEQ ID NO: 50)	AATGTTTTTGTGATGTTG (SEQ ID NO: 896)
3	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGCGAACGTTTGGG (SEQ ID NO: 899)
4	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGTGAATGTTTGGG (SEQ ID NO: 900)
5	CDH13 (SEQ ID NO: 50)	AAGGAATTCGTTTTGTAA (SEQ ID NO: 903)
6	CDH13 (SEQ ID NO: 50)	AAGGAATTTGTTTTGTAA (SEQ ID NO: 904)
7	CSPG2 (SEQ ID NO: 21)	GGGTAACGTCGAATTTAG (SEQ ID NO: 901)
8	CSPG2 (SEQ ID NO: 21)	GGGTAATGTTGAATTTAG (SEQ ID NO: 902)
9	CD44 (SEQ ID NO: 20)	TTGTTTAGCGGATTTTAG (SEQ ID NO: 897)
10	CD44 (SEQ ID NO: 20)	TTGTTTAGTGGATTTTAG (SEQ ID NO: 898)
11	EYA4 (SEQ ID NO: 24)	AGTGTATGCGTAGAAGGT (SEQ ID NO: 923)
12	EYA4	AGTGTATGTGTAGAAGGT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 24)	(SEQ ID NO: 924)
13	APC (SEQ ID NO: 12)	TTTAATCGTATAGTTTGT (SEQ ID NO: 971)
14	APC (SEQ ID NO: 12)	TTTAATTGTATAGTTTGT (SEQ ID NO: 972)
15	PTGS2 (SEQ ID NO: 52)	TTTATTTTCGTGGGTAAA (SEQ ID NO: 913)
16	PTGS2 (SEQ ID NO: 52)	TTTATTTTTGTGGGTAAA (SEQ ID NO: 914)
17	EYA4 (SEQ ID NO: 24)	AAGTAAGTCGTTGTTGTT (SEQ ID NO: 921)
18	EYA4 (SEQ ID NO: 24)	AAGTAAGTTGTTGTTGTT (SEQ ID NO: 922)
19	PTEN (SEQ ID NO: 39)	ATTTTGCGTTCGTATTTA (SEQ ID NO: 987)
20	PTEN (SEQ ID NO: 39)	ATTTTGTGTTTGTATTTA (SEQ ID NO: 988)
21	GSTP1 (SEQ ID NO: 25)	GGAGTTCGCGGGATTTTT (SEQ ID NO: 905)
22	GSTP1 (SEQ ID NO: 25)	GGAGTTTGTGGGATTTTT (SEQ ID NO: 906)
23	CAV1 (SEQ ID NO: 49)	TAGATTCGGAGGTAGGTA (SEQ ID NO: 911)
24	CAV1 (SEQ ID NO: 49)	TAGATTTGGAGGTAGGTA (SEQ ID NO: 912)
25	EGFR (SEQ ID NO: 23)	ATTTGGTTCGATTTGGAT (SEQ ID NO: 931)
26	EGFR (SEQ ID NO: 23)	ATTTGGTTTGATTTGGAT (SEQ ID NO: 932)
27	N33 (SEQ ID NO: 36)	TGTTATTTCGGAGGGTTT (SEQ ID NO: 909)
28	N33 (SEQ ID NO: 36)	TGTTATTTTGGAGGGTTT (SEQ ID NO: 910)
29	IGF2 (SEQ ID NO: 29)	TTGTATGGTCGAGTTTAT (SEQ ID NO: 941)
30	IGF2 (SEQ ID NO: 29)	TTGTATGGTTGAGTTTAT (SEQ ID NO: 942)
31	HLA-F (SEQ ID NO: 10)	AGTTGTTTCGTAGATATT (SEQ ID NO: 989)
32	HLA-F (SEQ ID NO: 10)	AGTTGTTTTGTAGATATT (SEQ ID NO: 990)
33	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTACGGGTTGGAG (SEQ ID NO: 917)
34	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTATGGGTTGGAG (SEQ ID NO: 918)
35	TP73 (SEQ ID NO: 46)	AAGTTACGGGTTTTATTG (SEQ ID NO: 915)
36	TP73	AAGTTATGGGTTTTATTG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 46)	(SEQ ID NO: 916)

Table 5: Oligonucleotides used in differentiation between colon adenoma tissue and healthy colon tissue.

No:	*Gene*	*Oligo:*
1	CD44 (SEQ ID NO: 20)	TTGTTTAGCGGATTTTAG (SEQ ID NO: 897)
2	CD44 (SEQ ID NO: 20)	TTGTTTAGTGGATTTTAG (SEQ ID NO: 898)
3	HLA-F (SEQ ID NO: 10)	TATTTGGGCGGGTGAGTG (SEQ ID NO: 939)
4	HLA-F (SEQ ID NO: 10)	TATTTGGGTGGGTGAGTG (SEQ ID NO: 940)
5	TGFBR2 (SEQ ID NO: 43)	AAAGTTTTCGGAGGGGTT (SEQ ID NO: 907)
6	TGFBR2 (SEQ ID NO: 43)	AAAGTTTTTGGAGGGGTT (SEQ ID NO: 908)
7	GTBP/MSH6 (SEQ ID NO: 26)	GAGGAATTCGGGTTTTAG (SEQ ID NO: 951)
8	GTBP/MSH6 (SEQ ID NO: 26)	GAGGAATTTGGGTTTTAG (SEQ ID NO: 952)
9	GTBP/MSH6 (SEQ ID NO: 26)	TTTGTTGGCGGGAAATTT (SEQ ID NO: 925)
10	GTBP/MSH6 (SEQ ID NO: 26)	TTTGTTGGTGGGAAATTT (SEQ ID NO: 926)
11	LKB1 (SEQ ID NO: 30)	AGGGAGGTCGTTGGTATT (SEQ ID NO: 933)
12	LKB1 (SEQ ID NO: 30)	AGGGAGGTTGTTGGTATT (SEQ ID NO: 934)
13	CD44 (SEQ ID NO: 20)	GTGGGGTTCGGAGGTATA (SEQ ID NO: 919)
14	CD44 (SEQ ID NO: 20)	GTGGGGTTTGGAGGTATA (SEQ ID NO: 920)
15	N33 (SEQ ID NO: 36)	GTTTAGTTAGCGGGTTTT (SEQ ID NO: 943)
16	N33 (SEQ ID NO: 36)	GTTTAGTTAGTGGGTTTT (SEQ ID NO: 944)
17	CDH13 (SEQ ID NO: 50)	AATGTTTTCGTGATGTTG (SEQ ID NO: 895)
18	CDH13 (SEQ ID NO: 50)	AATGTTTTTGTGATGTTG (SEQ ID NO: 896)
19	TP73 (SEQ ID NO: 46)	AAGTTACGGGTTTTATTG (SEQ ID NO: 915)
20	TP73 (SEQ ID NO: 46)	AAGTTATGGGTTTTATTG (SEQ ID NO: 916)
21	PTEN (SEQ ID NO: 39)	TGATGTGGCGGGATTTTT (SEQ ID NO: 947)
22	PTEN	TGATGTGGTGGGATTTTT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 39)	(SEQ ID NO: 948)
23	N33 (SEQ ID NO: 36)	TGTTATTTCGGAGGGTTT (SEQ ID NO: 909)
24	N33 (SEQ ID NO: 36)	TGTTATTTTGGAGGGTTT (SEQ ID NO: 910)
25	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGCGAACGTTTGGG (SEQ ID NO: 899)
26	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	AATTTGTGAATGTTTGGG (SEQ ID NO: 900)
27	GSTP1 (SEQ ID NO: 25)	GGAGTTCGCGGGATTTTT (SEQ ID NO: 905)
28	GSTP1 (SEQ ID NO: 25)	GGAGTTTGTGGGATTTTT (SEQ ID NO: 906)
29	EGFR (SEQ ID NO: 23)	TTTGTATTCGGAGTTGGG (SEQ ID NO: 961)
30	EGFR (SEQ ID NO: 23)	TTTGTATTTGGAGTTGGG (SEQ ID NO: 962)
31	RARB (SEQ ID NO: 40)	TAGTAGTTCGGGTAGGGT (SEQ ID NO: 991)
32	RARB (SEQ ID NO: 40)	TAGTAGTTTGGGTAGGGT (SEQ ID NO: 992)
33	N33 (SEQ ID NO: 36)	ATTTAGTTCGGGGGAGGA (SEQ ID NO: 993)
34	N33 (SEQ ID NO: 36)	ATTTAGTTTGGGGGAGGA (SEQ ID NO: 994)
35	CAV1 (SEQ ID NO: 49)	TAGATTCGGAGGTAGGTA (SEQ ID NO: 911)
36	CAV1 (SEQ ID NO: 49)	TAGATTTGGAGGTAGGTA (SEQ ID NO: 912)
37	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTACGGGTTGGAG (SEQ ID NO: 917)
38	TPEF (=TMEFF2; =HPP1) (SEQ ID NO: 54)	ATAGGTTATGGGTTGGAG (SEQ ID NO: 918)
39	CDKN2a (SEQ ID NO: 18)	AATAGTTACGGTCGGAGG (SEQ ID NO: 981)
40	CDKN2a (SEQ ID NO: 18)	AATAGTTATGGTTGGAGG (SEQ ID NO: 982)
41	N33 (SEQ ID NO: 36)	TTGGTTCGGGAAAGGTAA (SEQ ID NO: 977)
42	N33 (SEQ ID NO: 36)	TTGGTTTGGGAAAGGTAA (SEQ ID NO: 978)
43	MLH1 (SEQ ID NO: 32)	TTAGGTAGCGGGTAGTAG (SEQ ID NO: 949)
44	MLH1 (SEQ ID NO: 32)	TTAGGTAGTGGGTAGTAG (SEQ ID NO: 950)
45	APC	TATTTTGGCGGGTTGTAT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 12)	(SEQ ID NO: 985)
46	APC (SEQ ID NO: 12)	TATTTTGGTGGGTTGTAT (SEQ ID NO: 986)
47	CSPG2 (SEQ ID NO: 21)	GGGTAACGTCGAATTTAG (SEQ ID NO: 901)
48	CSPG2 (SEQ ID NO: 21)	GGGTAATGTTGAATTTAG (SEQ ID NO: 902)
49	CDH1 (SEQ ID NO: 15)	TAGTGGCGTCGGAATTGT (SEQ ID NO: 929)
50	CDH1 (SEQ ID NO: 15)	TAGTGGTGTTGGAATTGT (SEQ ID NO: 930)
51	PTGS2 (SEQ ID NO: 52)	TTTATTTTCGTGGGTAAA (SEQ ID NO: 913)
52	PTGS2 (SEQ ID NO: 52)	TTTATTTTTGTGGGTAAA (SEQ ID NO: 914)
53	RASSF1 (SEQ ID NO: 62)	TTTGTAGCGGGTGGAGTA (SEQ ID NO: 995)
54	RASSF1 (SEQ ID NO: 62)	TTTGTAGTGGGTGGAGTA (SEQ ID NO: 996)
55	WT1 (SEQ ID NO: 9)	TATATTGGCGAAGGTTAA (SEQ ID NO: 967)
56	WT1 (SEQ ID NO: 9)	TATATTGGTGAAGGTTAA (SEQ ID NO: 968)
57	CDKN2a (SEQ ID NO: 18)	GGAGTTTTCGGTTGATTG (SEQ ID NO: 997)
58	CDKN2a (SEQ ID NO: 18)	GGAGTTTTTGGTTGATTG (SEQ ID NO: 998)
59	ESR1 (SEQ ID NO: 60)	TGGAGGTTCGGGAGTTTA (SEQ ID NO: 969)
60	ESR1 (SEQ ID NO: 60)	TGGAGGTTTGGGAGTTTA (SEQ ID NO: 970)
61	IGF2 (SEQ ID NO: 29)	GATTAGGGCGGGAAATAT (SEQ ID NO: 937)
62	IGF2 (SEQ ID NO: 29)	GATTAGGGTGGGAAATAT (SEQ ID NO: 938)
63	MYOD1 (SEQ ID NO: 8)	AATTAGGTCGGATAGGAG (SEQ ID NO: 975)
64	MYOD1 (SEQ ID NO: 8)	AATTAGGTTGGATAGGAG (SEQ ID NO: 976)
65	CDH13 (SEQ ID NO: 50)	AAGGAATTCGTTTTGTAA (SEQ ID NO: 903)
66	CDH13 (SEQ ID NO: 50)	AAGGAATTTGTTTTGTAA (SEQ ID NO: 904)
67	EGR4 (SEQ ID NO: 4)	GGAGTTTTCGGTATATAT (SEQ ID NO: 927)
68	EGR4 (SEQ ID NO: 4)	GGAGTTTTTGGTATATAT (SEQ ID NO: 928)
69	S100A2 (SEQ ID NO: 42)	TATGTATACGAGTATTGG (SEQ ID NO: 999)
70	S100A2	TATGTATATGAGTATTGG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 42)	(SEQ ID NO: 1000)
71	DAPK1 (SEQ ID NO: 22)	TTGTTTTTCGGAAATTTG (SEQ ID NO: 935)
72	DAPK1 (SEQ ID NO: 22)	TTGTTTTTTGGAAATTTG (SEQ ID NO: 936)
73	MGMT (SEQ ID NO: 31)	AGTAGGATCGGGATTTTT (SEQ ID NO: 1001)
74	MGMT (SEQ ID NO: 31)	AGTAGGATTGGGATTTTT (SEQ ID NO: 1002)
75	EYA4 (SEQ ID NO: 24)	AAGTAAGTCGTTGTTGTT (SEQ ID NO: 921)
76	EYA4 (SEQ ID NO: 24)	AAGTAAGTTGTTGTTGTT (SEQ ID NO: 922)
77	CEA (SEQ ID NO: 56)	AAGTGTTCGCGGTTGTTT (SEQ ID NO: 1003)
78	CEA (SEQ ID NO: 56)	AAGTGTTTGTGGTTGTTT (SEQ ID NO: 1004)
79	WT1 (SEQ ID NO: 9)	TGTTATATCGGTTAGTTG (SEQ ID NO: 959)
80	WT1 (SEQ ID NO: 9)	TGTTATATTGGTTAGTTG (SEQ ID NO: 960)
81	GPIb beta (SEQ ID NO: 7)	GGAGTTCGGTCGGGTTTT (SEQ ID NO: 1005)
82	GPIb beta (SEQ ID NO: 7)	GGAGTTTGGTTGGGTTTT (SEQ ID NO: 1006)
83	CALCA (SEQ ID NO: 14)	ATTAGGTTCGTGTTTTAG (SEQ ID NO: 953)
84	CALCA (SEQ ID NO: 14)	ATTAGGTTTGTGTTTTAG (SEQ ID NO: 954)
85	PTGS2 (SEQ ID NO: 52)	AGTTATTTCGTTATATGG (SEQ ID NO: 1007)
86	PTGS2 (SEQ ID NO: 52)	AGTTATTTTGTTATATGG (SEQ ID NO: 1008)
87	MYOD1 (SEQ ID NO: 8)	GTGTTAGTCGTTTAGGGT (SEQ ID NO: 1009)
88	MYOD1 (SEQ ID NO: 8)	GTGTTAGTTGTTTAGGGT (SEQ ID NO: 1010)
89	EYA4 (SEQ ID NO: 24)	AGTGTATGCGTAGAAGGT (SEQ ID NO: 923)
90	EYA4 (SEQ ID NO: 24)	AGTGTATGTGTAGAAGGT (SEQ ID NO: 924)
91	CSPG2 (SEQ ID NO: 21)	AAAAATTCGCGAGTTTAG (SEQ ID NO: 945)
92	CSPG2 (SEQ ID NO: 21)	AAAAATTTGTGAGTTTAG (SEQ ID NO: 946)
93	PGR (SEQ ID NO: 38)	TTAAGTGTCGGATTTGTG (SEQ ID NO: 1011)
94	PGR (SEQ ID NO: 38)	TTAAGTGTTGGATTTGTG (SEQ ID NO: 1012)
95	PCNA	TAAAGAGGCGGGGAGATT

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 58)	(SEQ ID NO: 1013)
96	PCNA (SEQ ID NO: 58)	TAAAGAGGTGGGGAGATT (SEQ ID NO: 1014)
97	MSH3 (SEQ ID NO: 34)	AGTATTTTCGTTTGAGGA (SEQ ID NO: 1015)
98	MSH3 (SEQ ID NO: 34)	AGTATTTTTGTTTGAGGA (SEQ ID NO: 1016)
99	WT1 (SEQ ID NO: 9)	TAGTGAGACGAGGTTTTT (SEQ ID NO: 1017)
100	WT1 (SEQ ID NO: 9)	TAGTGAGATGAGGTTTTT (SEQ ID NO: 1018)
101	MYC (SEQ ID NO: 35)	TTATAATGCGAGGGTTTG (SEQ ID NO: 1019)
102	MYC (SEQ ID NO: 35)	TTATAATGTGAGGGTTTG (SEQ ID NO: 1020)
103	HIC-1 (SEQ ID NO: 27)	TTTTAGAGCGTTAGGGTT (SEQ ID NO: 1021)
104	HIC-1 (SEQ ID NO: 27)	TTTTAGAGTGTTAGGGTT (SEQ ID NO: 1022)
105	PTGS2 (SEQ ID NO: 52)	ATATTTGGCGGAAATTTG (SEQ ID NO: 1023)
106	PTGS2 (SEQ ID NO: 52)	ATATTTGGTGGAAATTTG (SEQ ID NO: 1024)
107	EGFR (SEQ ID NO: 23)	ATTTGGTTCGATTTGGAT (SEQ ID NO: 931)
108	EGFR (SEQ ID NO: 23)	ATTTGGTTTGATTTGGAT (SEQ ID NO: 932)
109	LKB1 (SEQ ID NO: 30)	TTTAGGTTCGTAAGTTTA (SEQ ID NO: 965)
110	LKB1 (SEQ ID NO: 30)	TTTAGGTTTGTAAGTTTA (SEQ ID NO: 966)
111	IGF2 (SEQ ID NO: 29)	TTGTATGGTCGAGTTTAT (SEQ ID NO: 941)
112	IGF2 (SEQ ID NO: 29)	TTGTATGGTTGAGTTTAT (SEQ ID NO: 942)
113	PTEN (SEQ ID NO: 39)	AGAGTTATCGTTTTGTTT (SEQ ID NO: 957)
114	PTEN (SEQ ID NO: 39)	AGAGTTATTGTTTTGTTT (SEQ ID NO: 958)
115	BCL2 (SEQ ID NO: 13)	TTTTGTTACGGTGGTGGA (SEQ ID NO: 1025)
116	BCL2 (SEQ ID NO: 13)	TTTTGTTATGGTGGTGGA (SEQ ID NO: 1026)
117	AR (SEQ ID NO: 5)	AGAGGTTGCGTTTTAGAG (SEQ ID NO: 1027)
118	AR (SEQ ID NO: 5)	AGAGGTTGTGTTTTAGAG (SEQ ID NO: 1028)
119	CDH1 (SEQ ID NO: 15)	AGGGTTATCGCGTTTATG (SEQ ID NO: 983)
120	CDH1	AGGGTTATTGTGTTTATG

No:	*Gene*	*Oligo:*
	(SEQ ID NO: 15)	(SEQ ID NO: 984)

Table 6: Oligonucleotides used in differentiation between colon carcinoma tissue and colon adenoma tissue.

No:	*Gene*	*Oligo:*
1	CDKN2a (SEQ ID NO: 18)	GTTGTTTTCGGTTGGTGT (SEQ ID NO: 1029)
2	CDKN2a (SEQ ID NO: 18)	GTTGTTTTTGGTTGGTGT (SEQ ID NO: 1030)
3	GPIb beta (SEQ ID NO: 7)	GGAGTTCGGTCGGGTTTT (SEQ ID NO: 1005)
4	GPIb beta (SEQ ID NO: 7)	GGAGTTTGGTTGGGTTTT (SEQ ID NO: 1006)

Table 7: Crossreference table to relate numbers used in figure labelling to ID numbers used throughout the document

Number in Figures	Gene name
Healthy vs Non-Healthy	
50-D	CDH13
20-C	CD44
54-C	TPEF (=TMEFF2; =HPP1)
21-C	CSPG2
50-C	CDH13
25-B	GSTP1
43-C	TGFBR2
36-B	N33
49-A	CAV1
52-C	PTGS2
46-A	TP73
54-B	TPEF (=TMEFF2; =HPP1)
20-A	CD44
24-D	EYA4
24-B	EYA4
26-B	GTBP/MSH6
4-C	EGR4
15-E	CDH1
23-E	EGFR
30-B	LKB1
22-D	DAPK1
29-D	IGF2
10-A	HLA-F
29-C	IGF2
36-C	N33
21-D	CSPG2
39-D	PTEN
32-B	MLH1
26-A	GTBP/MSH6

14-C	CALCA
22-C	DAPK1
39-C	PTEN
9-D	WT1
23-A	EGFR
21-A	CSPG2
30-A	LKB1
9-C	WT1
60-E	ESR1
12-A	APC
29-A	IGF2
8-D	MYOD1
36-A	N33
54-A	TPEF (=TMEFF2; =HPP1)
18-E	CDKN2a
15-D	CDH1
12-C	APC
Healthy vs Carcinoma	
50-D	CDH13
54-C	TPEF (=TMEFF2; =HPP1)
50-C	CDH13
21-C	CSPG2
20-C	CD44
24-B	EYA4
12-A	APC
52-C	PTGS2
24-D	EYA4
39-B	PGR
25-B	GSTP1
49-A	CAV1
23-E	EGFR
36-B	N33
29-C	IGF2
10-D	HLA-F
54-B	TPEF (=TMEFF2; =HPP1)
46-A	TP73
Healthy vs Adenoma	
20-C	CD44
10-A	HLA-F
43-C	TGFBR2
26-A	GTBP/MSH6
26-B	GTBP/MSH6
30-B	LKB1
20-A	CD44
36-C	N33
50-D	CDH13
46-A	TP73
39-D	PTEN

36-B	N33
54-C	TPEF (=TMEFF2; =HPP1)
25-B	GSTP1
23-A	EGFR
40-A	RARB
36-D	N33
49-A	CAV1
54-B	TPEF (=TMEFF2; =HPP1)
18-E	CDKN2a
36-A	N33
32-B	MLH1
12-C	APC
21-C	CSPG2
15-E	CDH1
52-C	PTGS2
62-D	RASSF1
9-C	WT1
18-D	CDKN2a
60-E	ESR1
29-D	IGF2
8-D	MYOD1
50-C	CDH13
4-C	EGR4
42-C	S100A2
22-D	DAPK1
31-E	MGMT
24-D	EYA4
56-A	CEA
9-D	WT1
7-E	GPIb beta
14-C	CALCA
52-D	PTGS2
8-B	MYOD1
24-B	EYA4
21-D	CSPG2
38-C	PGR
58-A	PCNA
34-D	MSH3
9-B	WT1
35-B	MYC
27-C	HIC-1
52-B	PTGS2
23-E	EGFR
30-A	LKB1
29-C	IGF2
39-C	PTEN
13-D	BCL2
5-B	AR
15-D	CDH1

Carcinoma vs Adenoma	
18-B	CDKN2a
7-E	GPIb beta

Patent Claims

1.A method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene and/or their regulatory regions from the group comprising MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F, ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR, EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2, ESR1, CASP8, RASSF1, MSH4, MSH5 in a subject, said method comprising contacting a target nucleic acid in a biological sample obtained from said subject with at least one reagent or a series of reagents, wherein said reagent or series of reagents, distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid.

2.A method according to claim 1 wherein, said method differentiates between normal colon tissue and colon cell proliferative disorder tissue.

3.A method according to claim 2 wherein, the method is carried out by means of methylation state analysis of genes from the group comprising APC, CALCA, CAV1, CD44, CDH1, CDH13, CDKN2a, CSPG2, DAPK1, EGFR , EGR4, ESR1, GSTP1, GTBP/MSH6, HLA-F, IGF2, LKB1, MLH1, MYOD1, N33, PTEN, PTGS2, TGFBR2, TP73, TPEF (=TMEFF2; =HPP1), WT1, and EYA4.

4.A method according to claim 1 wherein, said method differentiates between colon adenoma tissue and normal colon tissue.

5.A method according to claim 4 wherein, the method is carried out by means of methylation state analysis of genes from the group comprising APC, AR, BCL2, CALCA, CAV1, CD44, CDH1, CDH13, CDKN2a, CEA, CSPG2, DAPK1, EGFR, EGR4, ESR1, GPIb beta, GSTP1, GTBP/MSH6, HIC-1, HLA-F, IGF2, LKB1, MGMT, MLH1, MSH3, MYC, MYOD1, N33, PCNA, PGR, PTEN, PTGS2, RARB, RASSF1, S100A2, TGFBR2, TP73, TPEF (=TMEFF2; =HPP1), WT1, and EYA4.

6.A method according to claim 1 wherein, said method differentiates between colon carcinoma tissue and normal colon tissue.

7.A method according to claim 6 wherein, the method is carried out by means of methylation state analysis of genes from the group comprising APC, CAV1, CD44, CDH13, CSPG2, EGFR, GSTP1, HLA-F, IGF2, N33, PTEN, PTGS2, TP73, TPEF (=TMEFF2; =HPP1), and EYA4.

8.Use of methods according to claim 1 wherein, said methods are used to differentiate between colon adenoma tissue and colon carcinoma tissue.

9. A method according to claim 8 wherein, the method is carried out by means of methylation state analysis of genes from the group comprising GPIb beta and CDKN2a.

10. A method according to any one of Claims 1 to 9 comprising the following steps;

- obtaining a biological sample containing genomic DNA
- extracting the genomic DNA
- converting cytosine bases in the genomic DNA sample which are unmethylated at the 5-position, by treatment, to uracil or another base which is dissimilar to cytosine in terms of base pairing behaviour;
- fragments of the pretreated genomic DNA are amplified, and
- identification of the methylation status of one or more cytosine positions.

11.The method according to claim 10, characterised in that the reagent is a solution of bisulfite, hydrogen sulfite or disulfite.

12.The method as recited in Claims 10 and 11, characterised in that the amplification is carried out by means of the polymerase chain reaction (PCR).

13.The method as recited in one of the Claims 10 to 12, characterised in that the amplification is carried out by means of a heat-resistant DNA polymerase.

14.The method as recited in one of the Claims 10 to 13, characterised in that more than ten different fragments having a length of 100 - 2000 base pairs are amplified.

15. The method as recited in one of the Claims 10 to 14, wherein the amplification step is carried out using a set of primer oligonucleotides comprising SEQ ID NO: 389 to SEQ ID NO: 518.

16. The method as recited in one of the Claims 10 to 15, characterised in that the amplification of several DNA segments is carried out in one reaction vessel.

17. The method as recited in one of Claims 10 to 16, characterised in that the amplification step preferentially amplifies DNA which is of particular interest in healthy and/or diseased colon tissues, based on the specific genomic methylation status of colon tissue, as opposed to background DNA.

18. The method according to one of Claims 10 to 17, characterised in that the methylation status within at least one gene and/or their regulatory regions from the group comprising MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F, ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR , EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2, ESR1, CASP8, RASSF1, MSH4, and MSH5 is detected by hybridisation of each amplificate to an oligonucleotide or peptide nucleic acid (PNA)-oligomer.

19. A method according to claim 18, characterised in that the olignonucleotide or peptide nucleic acid (PNA)-oligomer is taken from the group comprising SEQ ID NO: 519 to SEQ ID NO: 1030.

20. The method according to Claims 10 to 19, characterised in that the amplificates are labelled.

21. The method as recited in Claim 20, characterised in that the labels of the amplificates are fluorescence labels.

22. The method as recited in Claim 20, characterised in that the labels of the amplificates are radionuclides.

23. The method as recited in Claims 20, characterised in that the labels of the amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer.

24. The method as recited in one of the Claims 10 to 23, characterised in that the amplificates or fragments of the amplificates are detected in the mass spectrometer.

25. The method as recited in one of the Claims 23 and 24, characterised in that the produced fragments have a single positive or negative net charge.

26. The method as recited in one of the Claims 23 to 25, characterised in that detection is carried out and visualized by means of matrix assisted laser desorption/ionisation mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI).

27. A method according to Claims 1 to 9 comprising the following steps;
   a) obtaining a biological sample containing genomic DNA
   b) extracting the genomic DNA
   c) digesting the genomic DNA comprising at least one or more CpGs of the genes MDR1, APOC2, CACNA1G, EGR4, AR, RB1, GPIb beta, MYOD1, WT1, HLA-F, ELK1, APC, BCL2, CALCA, CDH1, CDKN1A, CDKN1B (p27 Kip1), CDKN2a, CDKN2B, CD44, CSPG2, DAPK1, EGFR, EYA4, GSTP1, GTBP/MSH6, HIC-1, HRAS, IGF2, LKB1, MGMT, MLH1, MNCA9, MSH3, MYC, N33, PAX6, PGR, PTEN, RARB, SFN, S100A2, TGFBR2, TIMP3, TP53, TP73, VHL, CDKN1C, CAV1, CDH13, DRG1, PTGS2, THBS1, TPEF (=TMEFF2; =HPP1), DNMT1, CEA, MB, PCNA, CDC2, ESR1, CASP8, RASSF1, MSH4, and MSH5 with one or more methylation sensitive restriction enzymes, and
   d) detection of the DNA fragments generated in the digest of step c).

28. A method according to Claim 27, wherein the DNA digest is amplified prior to Step d).

29. The method as recited in Claim 28, characterised in that the amplification is carried out by means of the polymerase chain reaction (PCR).

30. The method as recited in one of the Claims 28 and/or 29, characterised in that the amplification of more than one DNA fragments is carried out in one reaction vessel.

31. The method as recited in one of the Claims 28 to 30, characterised in that the polymerase is a heat-resistant DNA polymerase.

32. An isolated nucleic acid of a pretreated genomic DNA according to one of the sequences taken from the group comprising SEQ ID NO: 133 to SEQ ID NO: 388 and sequences complementary thereto.

33. An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer, said oligomer comprising at least one base sequence of at least 10 nucleotides which hybridises to or is identical to a pretreated genomic DNA according to one of the SEQ ID NO: 133 to SEQ ID NO: 388 according to Claim 32.

34. The oligonucleotide as recited in Claim 33; wherein the base sequence includes at least one CpG or TpG dinucleotide sequence.

35. The oligonucleotide as recited in Claim 34; characterised in that the cytosine of the at least one CpG or TpG dinucleotide is/are located approximately in the middle third of the oligomer.

36. An oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer, according to one of the sequences taken from the group comprising SEQ ID NO: 519 to SEQ ID NO: 1030.

37.A set of oligonucleotides, comprising at least two oligonucleotides according to any of Claims 33 to 36.

38. A set of oligonucleotides, comprising at least two oligonucleotides according to SEQ ID NO: 895 to 986.

39. One or more isolated nucleic acid(s) taken from the group according to SEQ ID NO: 65 to 110.

40. A set of oligonucleotides, comprising at least two oligonucleotides according to SEQ ID NO: 895 to 906, 909 to 918, 921 to 924, 931, 932, 941, 942, 971, 972, and 987 to 990.

41. One or more isolated nucleic acid(s) taken from the group according to SEQ ID NO: 65 to 70, 72 to 76, 78, 79, 83, 88, 103, 111, and 112.

42. A set of oligonucleotides, comprising at least two oligonucleotides according to SEQ ID NO: 895 to 954, 957 to 962, 965 to 970, 975 to 978, 981 to 986, and 991 to 1028.

43. One or more isolated nucleic acid(s) taken from the group according to SEQ ID NO: 65 to 94, 96 to 98, 100 to 102, 105, 106, 108 to 110, and 113 to 131.

44. A set of oligonucleotides, comprising at least two oligonucleotides according to SEQ ID NO: 005, 1006, 1029, and 1030.

45. One or more isolated nucleic acid(s) taken from the group according to SEQ ID NO: 120, and 132.

46. A set of oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids as recited in Claims 37 to 45, comprising oligomers for detecting the methylation state of all CpG dinucleotides within one or more of the sequences according to SEQ ID NO: 1 to SEQ ID NO: 64 and sequences complementary thereto.

47. Use of a set of oligomers or peptide nucleic acid (PNA)-oligomers according to any of Claims 33 to 38, 40, 42, and 44 as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of sequences according to SEQ ID NO: 1 to SEQ ID NO: 64 and sequences complementary thereto.

48. Use of a set of oligonucleotides according to Claim 38 or nucleic acid(s) according to Claim 39 for the differentiation between colon adenoma or colon carcinoma tissue and normal colon tissue.

49. Use of a set of oligonucleotides according to Claim 40 or nucleic acid(s) according to Claim 41 for the differentiation between colon carcinoma tissue and normal colon tissue.

50. Use of a set of oligonucleotides according to Claim 42 or nucleic acid(s) according to Claim 43 for the differentiation between colon adenoma tissue and normal colon carcinoma.

51. Use of a set of oligonucleotides according to Claim 44 or nucleic acid(s) according to Claim 45 for the differentiation between colon carcinoma tissue and colon adenoma tissue.

52. A set of at least two oligonucleotides or peptide nucleic acid (PNA)-oligomers as recited in Claim 33, as primer oligonucleotides for the amplification of DNA sequences of one of SEQ ID NO: 133 to SEQ ID NO: 388 according to Claim 32 and/or sequences complementary thereto and segments thereof.

53.Use of a pretreated genomic DNA according to Claim 32 for the determination of the methylation status of a corresponding genomic DNA and/or detection of single nucleotide polymorphisms (SNPs).

54. A set of oligonucleotides or peptide nucleic acid (PNA)-oligomers as recited in Claims 37, 38, 40, 42 or 44, characterised in that at least one oligonucleotide is bound to a solid phase.

55. A set of oligonucleotides or peptide nucleic acid (PNA)-oligomers as recited in Claims 37, 38, 40, 42 or 44, characterised in that all members of the set are bound to a solid phase.

56. A method for manufacturing an arrangement of different oligomers or peptide nucleic acid (PNA)-oligomers (array) for analysing diseases associated with the corresponding genomic methylation status of the CpG dinucleotides within one of the SEQ ID NO: 1 to SEQ ID NO: 64 and sequences complementary thereto, wherein at least one oligomer according to any of the Claims 37, 38, 40, 42 or 44 is coupled to a solid phase.

57. An arrangement of different oligomers or peptide nucleic acid (PNA)-oligomers (array) obtainable according to claims 54 and 55.

58. An array of different oligonucleotide- and/or PNA-oligomer sequences as recited in Claim 57, characterised in that these are arranged on a plane solid phase in the form of a rectangular or hexagonal lattice.

59. A nucleic acid or peptide nucleic acid array for the analysis of colon cell proliferative disorders associated with the methylation state of genes comprising at least one nucleic acid according to one of the preceding claims.

60. The array as recited in any of the Claims 57 to 59, characterised in that the solid phase surface is composed of silicon, glass, polystyrene, aluminium, steel, iron, copper, nickel, silver, or gold.

61. A kit comprising a bisulfite (= disulfite, hydrogen sulfite) reagent as well as oligonucleotides and/or PNA-oligomers according to one of the Claims 33 to 46.

62. The use of oligonucleotides or peptide nucleic acid (PNA)-oligomers according to the groups of SEQ ID NO: 65 to SEQ ID NO: 132 and SEQ ID NO: 519 to SEQ ID NO: 1030 for the detection of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment, and/or monitoring of colon cell proliferative disorders.

63. A DNA sequence according to one of the sequences taken from the group comprising SEQ ID NO: 133 to SEQ ID NO: 388 and sequences complementary thereto for use in the analysis of cytosine methylation within said nucleic acid for the detection of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of colon cell proliferative disorders.

FIG 1

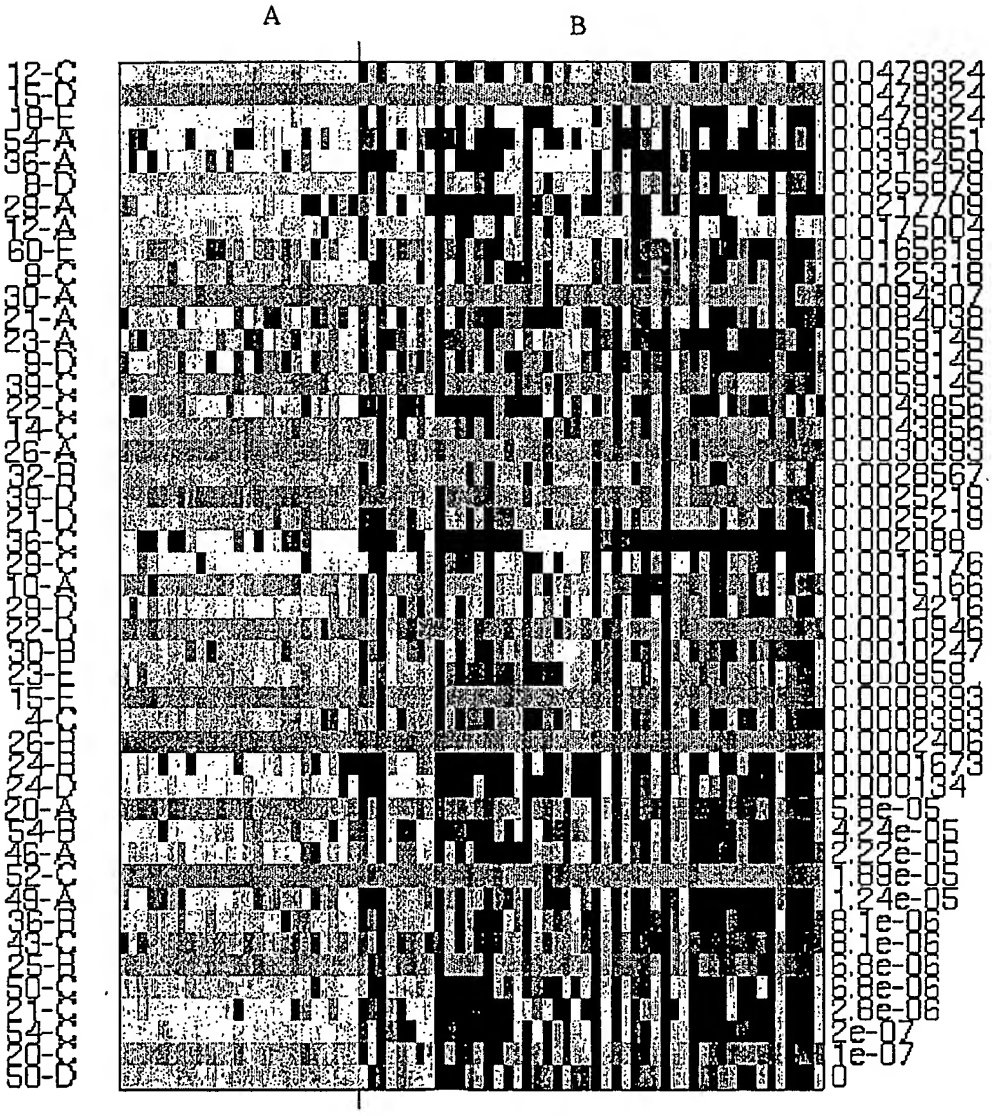
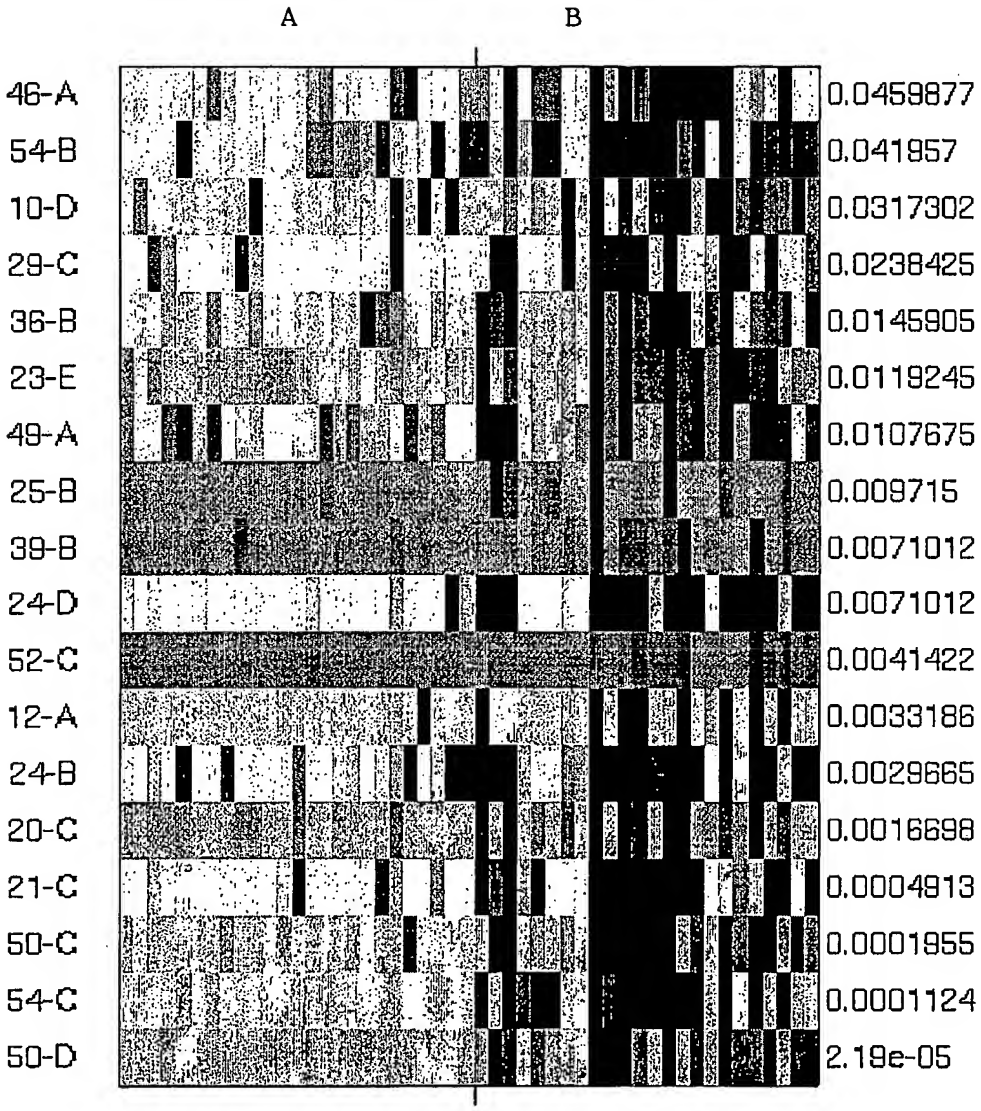


FIG 2


A
B
46-A
54-B
10-D
29-C
36-B
23-E
49-A
25-B
39-B
24-D
52-C
12-A
24-B
20-C
21-C
50-C
54-C
50-D
0.0459877
0.041957
0.0317302
0.0238425
0.0145905
0.0119245
0.0107675
0.009715
0.0071012
0.0071012
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0.0001955
0.0001124
2.19e-05

FIG 3

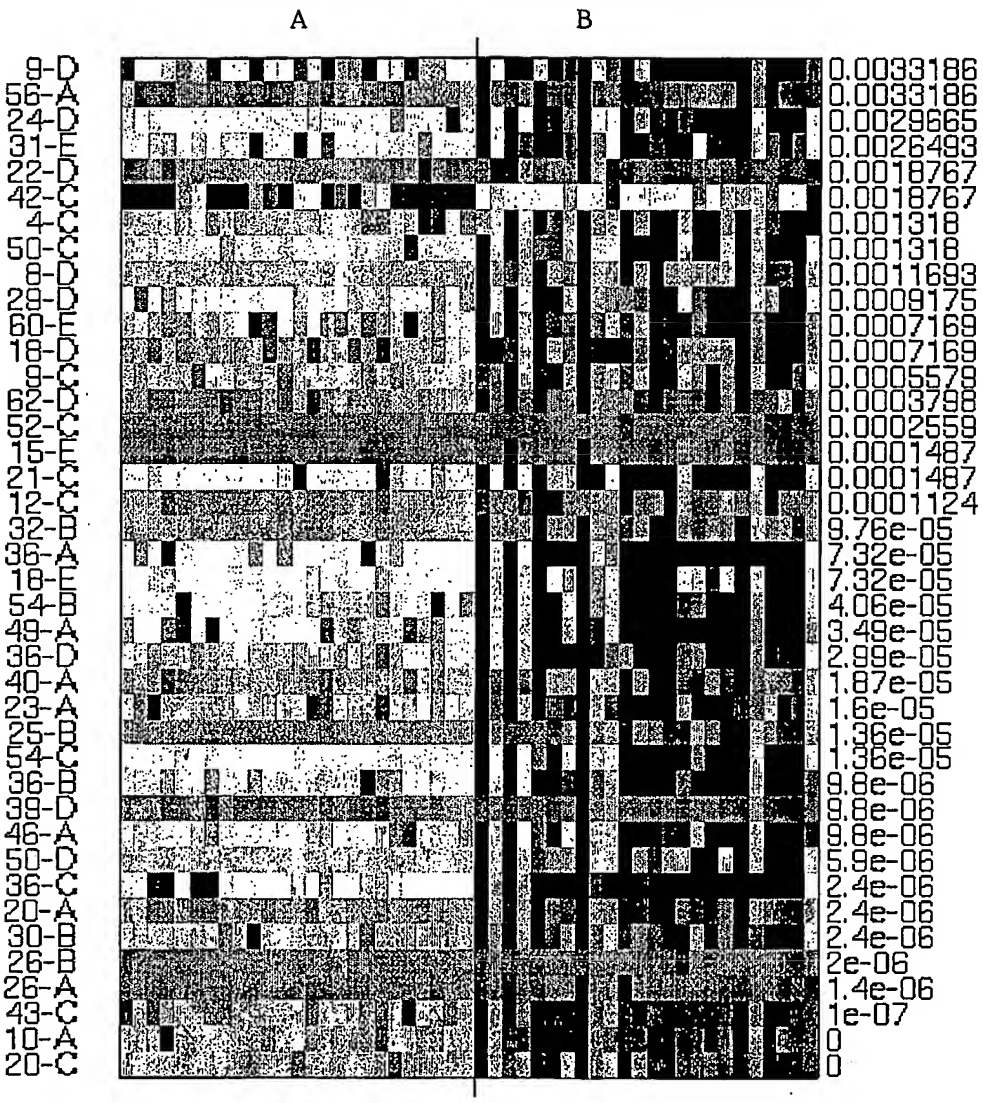
A
B
9-D 0.0033186
56-A 0.0033186
24-D 0.0029665
31-E 0.0026493
22-D 0.0018767
42-C 0.0018767
4-C 0.001318
50-C 0.001318
8-D 0.0011693
29-D 0.0009175
60-E 0.0007169
18-D 0.0007169
9-C 0.0005579
62-D 0.0003798
52-C 0.0002559
15-E 0.0001487
21-C 0.0001487
12-C 0.0001124
32-B 9.76e-05
36-A 7.32e-05
18-E 7.32e-05
54-B 4.06e-05
49-A 3.49e-05
36-D 2.99e-05
40-A 1.87e-05
23-A 1.6e-05
25-B 1.36e-05
54-C 1.36e-05
36-B 9.8e-06
39-D 9.8e-06
46-A 9.8e-06
50-D 5.9e-06
36-C 2.4e-06
20-A 2.4e-06
30-B 2.4e-06
26-B 2e-06
26-A 1.4e-06
43-C 1e-07
10-A 0
20-C 0

FIG 4